

GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 11:25:23 ; Search time 7565 Seconds

(without alignments)
262.559 Million cell updates/sec

Title: US-10-070-464-1
Perfect score: 4700
Sequence: 1 MAAMETBQLGVEIFETAD.....HLHYLQENLGRNALVKVI 882

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS-human40.cdi
-LIST=75 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=ptco -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4700	100.0	2671	24	ABK83322	CDNA encoding huma
2	4700	100.0	3106	24	ABK12892	Human protease PR
3	4700	100.0	3120	22	AAC85694	Nucleotide sequenc
4	4700	100.0	3120	24	AAD38856	Human dipeptidyl p
5	4700	100.0	3143	24	AAH99334	CDNA encoding 2195
6	4695	99.9	2643	24	AAH99335	Coding sequence of
7	4680	99.6	4829	24	ABK83327	CDNA encoding huma
8	4385.5	93.3	4685	24	ABK83332	CDNA encoding huma
9	4385	93.3	4676	24	ABK83331	CDNA encoding huma
10	4118	87.6	2842	24	ABK59774	Novel human coding
11	4092.5	87.1	4523	24	ABK83325	CDNA encoding huma
12	3970.5	84.5	2510	24	AAD23843	Human protease PR
13	3771	80.2	2668	24	ABK59775	Novel human coding
14	3661.5	77.9	4309	24	ABK83328	CDNA encoding huma
15	3364.5	71.6	2161	22	AAH15009	Human CDNA sequenc
16	2870	61.1	2617	24	ABK83323	CDNA encoding huma
17	2870	61.1	4219	24	ABK83335	CDNA encoding huma
18	2870	61.1	4302	24	ABK83333	CDNA encoding huma
19	2863	60.9	3024	24	AAD38954	Human dipeptidyl p
20	2835	60.3	2495	24	AAD38957	Human dipeptidyl p
21	2833	60.3	3287	24	AAD38855	Alternative versio
22	2820.5	60.0	4180	24	ABK83339	CDNA encoding huma
23	2820.5	60.0	4563	24	ABK83338	CDNA encoding huma
24	2763	58.8	2751	24	AAD38311	Murine dipeptidyl
25	2649	56.4	4076	24	ABK83337	CDNA encoding huma
26	2649	56.4	4159	24	ABK83336	CDNA encoding huma
27	2638	56.1	2801	22	AAI57896	Human polynucleoti
28	2599.5	55.3	4037	24	ABK83341	CDNA encoding huma
29	2599.5	55.3	4120	24	ABK83340	CDNA encoding huma
30	2476.5	52.7	3262	22	AAI57880	Human polynucleoti
31	2422	51.5	1669	22	AAC85966	Nucleotide sequenc
32	2226.5	47.4	2982	22	AAI59666	Human polynucleoti
33	2194.5	40.7	2461	21	AAC75835	Human ORF ORF190
34	1878.5	40.0	2952	24	ABK69090	DNA encoding huma
35	1874.5	39.9	3047	24	ABK69113	DNA encoding huma
36	1836.5	39.1	1083	22	AAC85697	Nucleotide sequenc
37	1645.5	35.0	1197	22	AAC85695	Nucleotide sequenc
38	1644.5	35.0	2027	21	AAC77137	Human ORF ORF2692
39	1599.5	34.0	3713	23	ABL10425	Drosophila melanog
40	1599.5	34.0	3783	23	ABL06641	Drosophila melanog
41	1400	29.8	2079	21	AAK37672	Human peptidase, H
42	1391	29.6	2411	24	ABK83334	CDNA encoding huma
43	1370.5	29.2	2034	22	AAI59682	Human polynucleoti
44	1360	28.9	6228	23	ABL10424	Drosophila melanog
45	1360	28.9	6228	23	ABL06640	Drosophila melanog
46	1351	28.7	1837	24	ABK69114	DNA encoding huma
47	1278	27.2	1356	24	ABK83326	CDNA encoding huma
48	1063	22.6	631	22	AAH07860	Human CDNA clone (
49	1026.5	21.8	832	24	ABK83330	CDNA encoding huma
50	929	19.8	873	22	AAE81719	Human protease and
51	927	19.7	925	24	ABL90148	Human polynucleoti
52	755.5	16.1	823	24	ABK30401	Human G-protein-co
53	736	15.7	1048	22	AA541004	Human CDNA 5'-end
54	668	14.2	662	22	AAK92083	Human CDNA clone r
55	668	14.2	662	22	AAK93366	Human full-length
56	668	14.2	1748	22	AAK94819	Human full-length
57	665.5	14.2	561	22	AAI00876	Human reproductive
58	597.5	12.7	2313	20	AAK00013	Aspergillus oryzae
59	597.5	12.7	5496	20	AAH07327	Aspergillus oryzae
60	572	12.2	2199	21	AAH57338	Nucleotide sequenc
61	529	11.3	3407	24	AAK92227	Prostate cancer-as
62	526	11.2	2924	15	AAO63261	CD26 CDNA clone.
63	525	11.2	2924	14	AAO46089	Sequence of human
64	524	11.1	4835	24	ABK63663	Rat sequence diffe
65	475.5	10.1	587	22	AAH12830	Human CDNA clone (
66	466.5	9.9	2505	23	ABL29869	Drosophila melanog
67	464	9.9	620	24	ABK83329	CDNA encoding huma

68	461	9.8	2388	24	ABA05888	Human aminopeptidase
69	461	9.8	2583	24	ABK83324	CDNA encoding human
70	461	9.8	3238	24	ABA05887	CDNA encoding human
71	461	9.8	4541	24	ABK83342	CDNA encoding human
72	456.5	9.7	2967	23	ABL17649	Drosophila melanog
73	455	9.7	3224	24	AA594862	Human DNA sequence
74	454	9.7	2814	24	ABL62162	Colon adenocarcinoma
75	454	9.7	2814	24	ABL63097	Breast cancer cell

ALIGNMENTS

RESULT 1
ABK83322 standard; CDNA; 2671 BP.

XX AC ABK83322:
XX 12-AUG-2002 (first entry)

XX DE CDNA encoding human DPPIV related serine protease DPP-1.

KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyslexia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.

XX OS Homo sapiens.

XX PN WO200231134-A2.

XX PD 18-APR-2002.

XX PF 12-OCT-2001; 2001WO-US31874.

XX PR 12-OCT-2000; 2000US-240117P.

XX (FERR) FERRING BV.

XX PI Qi S, Akinsanya KO, Riviere PJ, Junten J;

XX DR WPI: 2002-444178/47.

XX DR P-PSDB; ABG61591.

PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain

XX PS Claim 1: Page 53-54; 113pp; English.

CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypertension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyslexias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPPR proteins.

XX Sequence 2671 BP; 805 A; 524 C; 594 G; 748 T; 0 other;

Alignment Scores:

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Length:

2671

Score:	4700.00	Matches:	882
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-070-464-1 (1-882) x ABK83322 (1-2671)

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QY	21	GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr	40
DB	68	GAGGAGAAATATGAAACACAGCATCGCCCTAAATGGAGCCCTTTATGTCGCGAT	127
QY	41	SerTyrSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet	60
DB	128	TCTGGAGTCAGCTTAAAGCTGCTTGGCCGATACAGAAATATCATGCTCATGATG	187
QY	61	AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer	80
DB	188	GCTAAGGACACACATGATTTTCATGTTGTGACAGAGATATCCAGATGACCTCATTC	247
QY	81	AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer	100
DB	248	GACGAGATCTATTAACCTTGCCTGCTGAGAGACAGAAATATCACCTGTTTATCT	307
QY	101	GluIleProLysThrIleAsnArgAlaIleValLeuMetLeuSerTyrProLysLeu	120
DB	308	GAAATTCCTCAAACTATCATATAGAGCAGCTTATGCTCTTGGAGGCTCTTTTG	367
QY	121	AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg	140
DB	368	GATCTTTTCAGGACACACGACGATGAGATATTCGACAGAGACATATTAGA	427
QY	141	GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly	160
DB	428	GAAAGAAACGATTTGAGACAGTCGGAAATGCTTTCATCATATATCACCAAGAGTGA	487
QY	161	ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyProGlnGly	180
DB	488	ACATTTCTGTTCAAGCGGTAGTGAATTAACGCTAAAGATGAGGCGCACAGGA	547
QY	181	PheThrGlnLeuProLeuAspProAsnLeuValGluThrSerCysProAsnIleArgMet	200
DB	548	TTTACGCAACACCTTAAAGCCCATCTAGTGAAGTGTGTCACCAACATACGATG	607
QY	201	AspProLysLeuCysProAlaAspProAspTyrIleAlaPheIleHisSerAsnAspIle	220
DB	608	GATCCAAATTAATGCGCTGCTGATCCAGACTGATGCTTTTATACATACCAACGATATT	667
QY	221	TyrIleSerAsnIleValThrArgGluIleArgGluIleArgGluIleValHisAsnGluLeu	240
DB	668	TGATATATCAACATCGTAACAGAGAGAGAGAGACTCATATGCGCAATGAGCTA	727
QY	241	AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGln	260
DB	728	GCCACATGGAAGAAAGATGCGCATACGTCGAGTGGCTTGTTCACCAAGAAAGAA	787
QY	261	PheAspArgTyrSerGlyTyrTyrProCysProLysAlaGluThrThrProSerGlyGly	280
DB	788	TTTGATATGATATTCGTGCTATGTTGTGTGTCGCAAAAGCTGAAACATCCCATGGTGT	847
QY	281	LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleHisVal	300
DB	848	AAATATCTTAAGATCTATATGAGAAAGAAATCATGAACTGAGTGAATTAATTCATGTT	907
QY	301	ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysTyrGlnGlyThr	320
DB	908	ACATCCCTATGTTGGAACAGAGAGGACGATTCATTCGTTATCTTAACAGAGTACA	967
QY	321	AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle	340

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QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
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QY 501 GlyGluTrpGluValLeuGluLysArgHisGlySerAsnIleGlnValAspGluValArgArg 520
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QY 521 LeuValTyrPheGluGluIleThrLysAspSerProLeuGluHisIleLeuValIleSer 540
Db CTGGTATATTTGAGAGGACCAAGACCTCCCTTTAGACATCATCTGATGATGAT 1627
QY 541 TyrValAsnProGluGluValThrArgLeuThrAspArgGlyTyrSerHisSerCys 560
Db TACGTAAATCCTGAGAGAGTGACAAAGCTGACTGACCGTACTACATTCCTCTG 1687
QY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
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QY 581 ValSerLeuTyrLysLeuSerSerProGluAspProThrCysLysThrLysGluPhe 600
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QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
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Db 2048 TATGTGTTTACTGATAGACACAGGAGTCTGTACCGAGGCTTAAATTTGAAGC 2107
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Db CTAGCTTCGATATGATTTTCATTGACTTAGATCGTGGGATCCAGCGCTGCTCTAT 2227
QY 741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
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QY 761 AlaGlyAlaProValThrLeuTrpIlePheTyrAspThrGlyTyrThrGluArgTyrMet 780
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QY 781 GlnHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
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QY 801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
Db AAGTTCCTCTGAACCAATCGTTTACTGCTTACATGTTTCTCGATGAGAAATGTC 2467
QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
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QY 841 LeuGlnIleTyrProGlnArgHisSerIleArgValProGluSerGlyGlnHisTyr 860
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QY 861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaIleLeuLys 880
Db GAACCTCATCTTTTGCATCACTTCAAGAAACCTTGATACAGTATTTGCTGCTTAATA 2647
QY 881 ValIle 882
Db 2648 GTGATA 2653

RESULT 2
ABK12892
ID ABK12892 standard: cDNA: 3106 BP.
XX
AC ABK12892:
XX
DT 09-APR-2002 (first entry)
XX
DE Human protease PRS-9 cDNA sequence.
XX
KW Human; protease; PRS; gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis; ss.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT 203..2851
FT CDS /tag=a
FT FT /product="Human protease PRS-9"
XX
XX PN WO200198468-A2.
XX
XX PD 27-DEC-2001.
XX
XX PF 13-JUN-2001: 2001MO-US19178.
XX
XX PR 16-JUN-2000: 2000US-212336P.

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PR 22-JUN-2000: 200005-213955P.
 PR 29-JUN-2000: 200005-215396P.
 PR 07-JUL-2000: 200005-216821P.
 PR 14-JUL-2000: 200005-218946P.
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 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Yue H, Elliott VS, Gandhi AR, Lal P, Au-Young J, Tribouley CM;
 PI Deleage AM, Baughn MR, Nguyen DB, Lee EA, Hafalia A, Khan FA;
 PI Walla NK, Yao MG, Lu DM, Patterson C, Tang YT, Walsh RT;
 PI Azimzai Y, Lu Y, Rankumar J, Xu Y, Reddy R, Das D, Kearney L;
 PI Kallik DA;
 DR WPI: 2002-090437/12.
 DR P-SDB: AAU74749.
 XX
 PT Twenty one human proteases (referred to as PRS-1 to PRS-21), useful
 PT in the diagnosis, treatment and prevention of gastrointestinal (e.g.
 PT gastritis), cardiovascular (e.g. atherosclerosis) and cell
 PT proliferative (e.g. cancer) disorders -
 PS
 PS Claim 5; Page 166-167; 177pp; English.
 XX
 CC The present invention relates to twenty one new human proteases,
 CC referred to as PRS-1 to PRS-21. The PRS polynucleotides and
 CC polypeptides of the invention are useful in the diagnosis, treatment and
 CC prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and
 CC Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and
 CC myocardial infarction, autoimmune/inflammatory e.g. acquired
 CC immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell
 CC proliferative e.g. cancer, developmental e.g. Duchenne and Becker
 CC muscular dystrophy, epithelial e.g. dermatitis, neurological e.g.
 CC epilepsy and Alzheimer's disease and reproductive e.g. infertility and
 CC endometriosis disorders. Numerous other examples of each disorder are
 CC given in the specification. The present nucleic acid sequence encodes
 CC the human protease PRS-9 protein of the invention.
 XX
 SQ Sequence 3106 BP; 928 A; 633 C; 704 G; 841 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3106
 Score: 4700.00 Matches: 882
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
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 DB 203 ATGCACACAGCAATGGAACAGACACCTGGCTTGAGATATTGAAACGCGACGT 262
 QY 21 GluIuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 40
 DB 263 GAGGAGATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 322
 QY 41 SerTrpSerGluLeuLysLysLeuAlaAspThrArgLysTrpLysGlyTyrMetMet 60
 DB 323 TCCTGGAGTCAGCTTAAGAAGCTCTTGGCATACGAAATAATCATGCTATATG 382
 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
 DB 383 GCTAAGCCACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 442
 QY 81 AspArgLysTrpLysLysAlaMetSerGlyLysAsnArgLysAsnArgLysPheTyrSer 100
 DB 443 GACGAAATCTATTACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 502
 QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
 DB 503 GAATTCCTCAAACTATCATATAGAGACAGCACTTAAATGCTCTTGGAGCCCTTTTG 562

QY 121 AsPheGluAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
 DB 563 GATCTTTTCAGGCAACACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 622
 QY 141 GluArgLysArgLysGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 DB 623 GAAAGAAACGATTTGAAACAGTGGATTCCTTTCATGATTTTCACCAAGAGAGTGA 682
 QY 161 ThrPheLeuPheGluAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
 DB 683 ACATTTCTGTTTCAAGCCGAGTGAATTTATACGTAAAGATGAGAGGCCCAAGGA 742
 QY 181 PheThrGlnGluProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 DB 743 TTTACGCAACACCTTTAAGGCCCAATCTAGTGAACATGTTCCCAACATACGATG 802
 QY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAspIle 220
 DB 803 GATCCAAATTTATGCTCCGTCGATCCAGACTGATTCCTTTTATACATACCAAGATATT 862
 QY 221 TrpIleSerAsnIleValThrArgGluGluArgArgLeuThrTyrValHisAsnGluLeu 240
 DB 863 TGGATATCTAACATCTGTAACAGAGAAAGAGAGACTCACTTATGTCCACATGACTGA 922
 QY 241 AlaAsnMetGluGluAspAlaArgSerArgLysValAlaThrPheValLeuGlnGluGlu 260
 DB 923 GCCAATCTGGAAGAGATGCGCATGACGTGAGTCCCTACCTTGTTCCTCAAGAGAA 982
 QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
 DB 983 TTTGATGATTTTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1042
 QY 281 LysIleLeuArgLysLeuTyrGluGluAlaAsnAspLysSerGluValGluIleIleHisVal 300
 DB 1043 AAATTTCTTAACATCTATATGAGAAAGAAATGATCAATCTGAGTGGAGAAATTTATTCAGTT 1102
 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
 DB 1103 ACATCCCTATGTTGGAACAGAGAGGAGAGATTCATTCCTGTTAAACAGGTACA 1162
 QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluArgLys 340
 DB 1163 GCAATCTCTAAAGTCACCTTTAAGATGTCAGAAATTAATGATGATGATGATGATGATGAT 1222
 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 DB 1223 ATGATGTCATAGATTAAGAGAACTAATTCACCTTTGAGATTCATTTGAAAGGATTGAA 1282
 QY 361 TyrIleAlaArgAlaGlyTyrPheProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
 DB 1283 TATATTCCTCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342
 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
 DB 1343 CGCTCCAGACTGCTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1402
 QY 401 AspAspValMetGluArgGluArgLeuIleGluSerValProAspSerValThrProLeu 420
 DB 1403 GATGATGTTATGGAAG 1462
 QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
 DB 1463 ATATATCTATGAGAAACAGAGATCTGTAATATTCATGACATCACTTTCATGATTTT 1522
 QY 441 ProGlnSerHisGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 460
 DB 1523 CCCCAAGATCAGTTTC 1582
 QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
 DB 1583 CGTCATTTATACAAATTTATACATGATTTTAAAGAGAAAGCAATTAACATGACAGTGT 1642
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500

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Db 1643 GGGCTGCTCCTCCAGACGATTCATCAAGAGAGATAGCAATACCAGT 1702
Qy 501 G1YGLuPrpGLuValLeuGLyArgHisGLySerSnlLeglnValAspGLuValArgArg 520
Db 1703 GGGAAATGGGAAGTCTTGCGCCGCGCATGATCTAATATCCAAAGTTGATGAAGTCAGAGG 1762
Qy 521 LeuValTyrPheGLuGLyTrpLysAspSerProLeuGLuHisHsLeuTyrValValSer 540
Db 1763 CTGGTATATTTTGAAGCACCAGCAAGACTCCCTTTAGAGCATCCCTGCTACGTAGTCACT 1822
Qy 541 TyrValAsnProGLyGLuVal1ThrArgLeuThrAspArgGLyTyrSerHisSerCysCys 560
Db 1823 TACCTAATCTCGAGAGAGTGACAGACGCTGACTGACCTGGCTACTCATCTTCTGCTGC 1882
Qy 561 HLeSerGLnHisCysAspPhePheHLeSerLysTyrSerSnglnLysAspProHisCys 580
Db 1883 ATCAGTCAGACGTGTGCTCTTTATAGTAACTATAGTAAACAGAAATCCACACTGT 1942
Qy 581 ValSerLeuTyrLysLeuSerSerProGLuAspAspProThrCysLysThrLysGLuPhe 600
Db 1943 GTGTCCTTTACAAAGCATATCAAGTCCTGAAGATGACCCCACTTCCAAACAAAGCAATTT 2002
Qy 601 TrpAlaThrIleLeuAspSerAlaGLyProLeuProAspTyrThrProProGLuIlePhe 620
Db 2003 TGGGCCACACATTTTGATGACGAGTCCTCTCTGACTATACTCTCCAGAAATTTTC 2062
Qy 621 SerPheGLuSerThrThrArgLysPheThrLeuTyrGLyMetLeuTyrLysProHisAspLeu 640
Db 2063 TCTTTTAAAGTACTACTGATGATTTTACATGTATGGGATGCTTCAAGACCTCAGATCTA 2122
Qy 641 GLnProGLyLysLysTyrProThrValLeuPheIleTyrGLyGLyProGLnValGLnLeu 660
Db 2123 CAGCCTGGAAAGAAATCTCTACTGCTGTTCATATATGGTGGTCCCTCAGGTCACTTG 2182
Qy 661 ValAsnAsnArgPheLysGLyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGLy 680
Db 2183 GTGAATATGCGTTTAAAGAGTCACATATTTCCGCTTGAACTACCTCTCTCTAGGT 2242
Qy 681 TyrValValValValIleAspAsnArgGLySerCysHisAspGLyLeuLysPheGLuGLy 700
Db 2243 TATGTGTTGTAGTATGATACACACAGGGGATCTGTCAACGAGGGCTTAAATTTTGAAGGC 2302
Qy 701 AlaPheLysTyrLysMetGLyGLnIleGLuIleAspAspGLnValGLyGLyLeuGLnTyr 720
Db 2303 GCCTTAAATATAAATGGGCAATAGAAATATGACATCGATCGTGAAGGACTCTCAATAT 2362
Qy 721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGLyIleHisGLyTyrSerTyr 740
Db 2363 CTACCTTCTGATATGATTTTCATTTGATGATCGTGTGGCATCCACGCTGCTCAT 2422
Qy 741 GLyLysTyrLeuSerLeuMetAlaLeuMetGLnArgSerAspIlePheArgValAlaIle 760
Db 2423 GGAAGATACCTCTCCGATGCGCATTAATGACAGAGTCAGATATCTTCAGGGTGTCTATT 2482
Qy 761 AlaGLyValProVal1ThrLeuTrpIlePheTyrAspThrGLyTyrTrnGLuArgTyrMet 780
Db 2483 GCTGGGGCCCCAGTCACTGTGTGATCTTCTATATACAGATACAGGAACGTTATATG 2542
Qy 781 GLyHisProAspGLnAsnGLnGLyIleTyrTyrLeuGLySerValAlaMetGLnAlaGLu 800
Db 2543 GGTTCACCTCACGCAATGAACAGGGCTATTTACTTACGATCTGGCCATGCAACGCAAGAA 2602
Qy 801 LysPheProSerGLuProAsnArgLeuLeuLeuHisGLyPheLeuAspGLuAspVal 820
Db 2603 AAGTCCCTCTGACCAAAATCGTTTACTGCTTCTACATGGTTTCCGTGAGGAAATATGTC 2662
Qy 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGLyLysProTyrAsp 840
Db 2663 CATTTTCACATACCACTATATATCTAGTATTTTATAGAGGGCTGGAAAGCCATATGAT 2722
Qy 841 LeuGLnIleTyrProGLnGLuArgHisSerIleArgValProGLuSerGLyGLnHisTyr 860

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Db 2723 TTACAGATCTATCTCAGAGACACACAGCATTAAGACTTCTGTAATCGGAGAACATTAT 2782
Qy 861 GLuLeuHisLeuLeuHisTyrLeuGLnGLuAsnLeuGLySerArgIleAlaIleLeuLys 880
Db 2783 GAACGTGATCTTTTGGCACTTCTCAAGAAACCTTGATCAGTATTTGCTGTAAAA 2842
Qy 881 ValIle 882
Db 2843 GTGATA 2848

RESULT 3
AAC85694
ID AAC85694 standard; CDNA: 3120 BP.
XX
AC AAC85694:
XX
XX 29-JUN-2001 (first entry)
XX
XX Nucleotide sequence of human DPP8.
XX
KW Human; dipeptidyl aminopeptidase; DPP8; prolly oligopeptidase;
KW dipeptidyl peptidase; DPPIV; T cell; cleavage; diarrhoea;
KW growth hormone deficiency; glucose level; mucosal regeneration;
KW non-insulin dependent diabetes mellitus; glucose intolerance;
KW immunosuppression; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..2862
FT FT /*tag= a
FT FT /product= "Human DPP8"
XX
XX MO200119866-A1.
XX
XX 22-MAR-2001.
XX
XX 11-SEP-2000; 2000MO-AU01085.
XX
XX 10-SEP-1999; 99AU-0002762.
XX 18-FEB-2000; 2000AU-0005709.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Abbott CA, Gorell MD:
XX WPI: 2001-281520/29.
XX P-PSDB: AAB47187.
XX
XX New human dipeptidyl aminopeptidase (DPP8) useful for cleaving
XX substrates, identifying inhibitors of DPP8 catalytic activity which
XX have therapeutic uses, and for detecting activated T cells
XX
XX Claim 16; Fig 2; 78pp: English.
XX
XX This sequence encodes human dipeptidyl aminopeptidase (DPP8). DPP8
XX has substrate specificity for H-Ala-Pro-pNA, H-Gly-Pro-pNA and
XX H-Arg-Pro-pNA. Therefore, it is a prolly oligopeptidase and a
XX dipeptidyl peptidase, because it is capable of hydrolysing the
XX peptide bond C-terminal to Pro in each of these compounds. DPP8
XX is homologous with human DPPIV. DPP8 is useful for cleaving a
XX substrate, and for detecting an activated T cell which involves
XX measuring the level of DPP8 gene expression in a T cell. The level
XX of DPP8 expression is detected by detecting the amount of DPP8 RNA
XX in the cell. It is also useful for identifying a molecule capable
XX of inhibiting the cleavage of the substrate by DPP8. Molecules
XX identified as inhibiting DPP8 catalytic activity may be useful for
XX treating diarrhoea, growth hormone deficiency, lowering glucose levels
XX in non-insulin dependent diabetes mellitus and other disorders
XX involving glucose intolerance, enhancing mucosal regeneration and
XX as immunosuppressants.
XX
XX Sequence 3120 BP; 936 A; 637 C; 706 G; 841 T; 0 other;

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Alignment Scores:

Pred. No.:	0	Length:	3120
Score:	4700.00	Matches:	882
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-10-070-464-1 (1-882) x AAC85694 (1-3120).

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OY 1 MetAlaAlaMetGluThrGluGluLeuGluGluIlePheGluThrAlaAspCys 20
    |||||
Db 214 ATGCAGAGCAATGAAACAGAACAGACGCTGCTTGAATATTGAAACGCGACATG 273
OY 21 GluGluAsnIleGluSerGluAspArgProLysLeuGluProPheTyrValGluArgTyr 40
    |||||
Db 274 GAGGAGATATTGATATACAGAGATGCGCTAAATTGAGCTTTTATGTTGAGCGGTAT 333
OY 41 SerTrpSerGluLeuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
    |||||
Db 334 TCCTGAGATGAGCTTAAAGACGCTTCCGATACCGAAATATCATGCGCTACATGATG 393
OY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
    |||||
Db 394 GCTAAGGACACATGATTCATGTTGCTGAAGAGGAATGATCCAGATGACCTCATTTCA 453
OY 81 AsparGlyIleTyrIleuAlaMetSerGlyLysAsnArgLysAsnThrLeuPheTyrSer 100
    |||||
Db 454 GACGAAATCTTACCTTCCATGCTGCTGAGACAGAACGAAATACCTCTTTATTCT 513
OY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
    |||||
Db 514 GAAATTCCTCAAAACATCAATAGAGACAGACACTTAAATGCTCTCTGGAACCTCTTTTG 573
OY 121 AspleuPheGluAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
    |||||
Db 574 GATCTTTTTCAGGACACGCTGATGAAATGTAATCTCAGAAAGAACTATTAGA 633
OY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlySerGly 160
    |||||
Db 634 GAAAGAAACCCATTCGACACGTCGGAATTCCTTTCGATTCACCAAGGAAGTGA 693
OY 161 ThrPheLeuPheGluAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
    |||||
Db 694 ACATTTCTGTTTCAAGCGGAGTGAATTTATCAGTAAAGATGAGGGCCCAACAGA 753
OY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
    |||||
Db 754 TTTAGGCAACACCTTTAAGGCCCAATCTAGTGAAACTAGTTGCTCCCAACATACGGATG 813
OY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
    |||||
Db 814 GATCCAAATATTAATGCCCGCGATCCAGACGTCGATTCGCTTTATATACAGACGATATT 873
OY 221 TrpIleSerAsnIleValThrArgGluGluArgLeuThrTyrValHisAsnGluLeu 240
    |||||
Db 874 TGGTATCTTAACATCTGATACAGAGAAAGAGAGACTCATTATGTGCACAAATGAGCTA 933
OY 241 AlaAsnMetGluLysAspAlaArgSerAlaGlyValAlaThrPheValLeuGluGlu 260
    |||||
Db 934 GCCAACATGGAAGAGATGCGATGACGTCGAGTCCGTACCTTTGTTCTCCAGAAAGAA 993
OY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
    |||||
Db 994 TTTCATATGATTTCTGCTGCTATGCTGCTGCTCAAAAGCTGAAACACCTCCAGTCGTCGT 1053
OY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
    |||||
Db 1054 AAAATTCCTTAACATCTATATGAGAAAGAAATGATGAATCTGAGTGAATATTATCATGTT 1113
OY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
    |||||
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Db 1114 ACATCCCTATGTTGGAACACAGAGGACAGATTCCGTTATCCTAAGAACAGTACA 1173
OY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluArgIle 340
    |||||
Db 1174 GCAATTCCTTAAGTACTTATTAAAGATGTCAGAAATATGATGATGCTGAAGAGGATTC 1233
OY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
    |||||
Db 1234 ATAGATGTCATAGADTAAGACACTAATTCACCTTTTGAGATTCTATTGGAAGAGTTGAA 1293
OY 361 TyrIleAlaArgAlaGlyTyrThrProGluLysTyrAlaTrpSerIleLeuLeuAsp 380
    |||||
Db 1294 TATATGCGACAGCTGATGACCTCCGAGGAAATATGCTGCTCATCCTACTGAT 1353
OY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
    |||||
Db 1354 CGCTCCGAGCTCCGCTTACATATGTTGATGCTCAGCTGATTTATTATCCAGTGA 1413
OY 401 AspAspValMetGluArgGluArgLeuIleGluSerValProAspSerValThrProLeu 420
    |||||
Db 1414 GATGATGTTATGGAAGGACAGACTCATTTGATGACAGCTGATTCGTGACGCCACTA 1473
OY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
    |||||
Db 1474 ATTAATCTATGAAGAACACACAGACATCTGATTAATATCCATGACATCTTTCATGTTTT 1533
OY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGlyCysLysThrGlyPhe 460
    |||||
Db 1534 CCCAAAGCTCAGAAAGAGAAATGATTTATTTTGCTCTGATGCAAAACAGGTTTC 1593
OY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
    |||||
Db 1594 CGTCATTTATACAAATATACATCTATTATTAAGGAAGCAAAATATTAACGATCCAGTGT 1653
OY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
    |||||
Db 1654 GGGCTGCTGCTCCAGAGATTTCAAGTCTCTATCAAGAGGAGATTAACCATCAGT 1713
OY 501 GlyLeuTrpGluValIleGluArgHisGlySerAsnIleGlnValAspGluValArg 520
    |||||
Db 1714 GGTGATGGAAGATCTTGGCGGCGATGATCTATATCCAAAGTTGATGAAGTACGAAG 1773
OY 521 LeuValTyrPheGluGlyThrLysAspSerProLeuGlnHisLysLeuTyrValIleSer 540
    |||||
Db 1774 CTGCTATATTTTGAAGCACCACCAAGACTCCCTTTAAGACATCACCTGATGATAGT 1833
OY 541 TyrValAsnProGluGluValThrArgLeuThrAspArgGlyTyrSerHisSerCys 560
    |||||
Db 1834 TACGTAATCTCTGAGAGAGTGACAAAGCTGACTGACCTGCTACATCTTTCGCTGC 1893
OY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
    |||||
Db 1894 ATCAGTCAGCAGCTGACTTCTTATAGTATAGTATAGTAAACGAAATCCACTGCT 1953
OY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
    |||||
Db 1954 GTGTCCCTTTCAAGCTATACAAAGTCTGAAGATACCCCAACTGTCACAAACAAAGAAATTT 2013
OY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuArgProAspTyrThrProProGluIlePhe 620
    |||||
Db 2014 TGGGCACCATTTTGGATGTCAGAGTCCCTCTCTCACTATACCTCCCGAAATTTTC 2073
OY 621 SerPheGluSerThrThrGluPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
    |||||
Db 2074 TCTTTTGAATACTACTGATTTACATTTGATGGATGCTCTCAAGACCTCATGATCTA 2133
OY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
    |||||
Db 2134 CAGCCTGGAAGAAATATCTCTACTGCTGCTGTATATATAGTGCTGCTCAGGTCAGATTG 2193
OY 661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
    |||||
Db 2194 GTGAATATCGCTTTAAAGAGTCAAGTATTTCCGCTTGGAATACCTAGCCTCTAGCT 2253
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QY 681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
    |||||||
Db 2254 TATGTGTTGTTAGTATGACACACAGGGGATCCGTGCACGAGGCGTTAAATTGAAGGC 2313
QY 701 AlapheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
    |||||||
Db 2314 GCCTTTAAATATATAAAGGTCACAAATAGAAATGACATCAGGTGGAAGGACTCCAAATAT 2373
QY 721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrSerTyr 740
    |||||||
Db 2374 CTAGCTTCTCGATATGATTTTCATTGACTTATGATGCTGTGGGACATCCAGCGTGTCTAT 2433
QY 741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
    |||||||
Db 2434 GGAGGATACCTCTCCCTGATGGCATTAATGCAGAGTCAGATATCTTCAGGCTGTATAT 2493
QY 761 AlagGlyAlaProValThrLeuThrPhePheTyrAspPheArgGlyTyrThrGluArgTyrMet 780
    |||||||
Db 2494 GCTGGGGCCCAAGTCACTGTGTGATCTTCTATGATACAGATACAGGAAACGTTATATG 2553
QY 781 GlyHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
    |||||||
Db 2554 GGTACCCCTGACCGATGAAACAGGCTATTACTTAGGATCTGTGGCATGCACAGAA 2613
QY 801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
    |||||||
Db 2614 AAGTTCCTCTGAAACCAATCGTTACTCTTACATGGTTTCCTGATGAGAAATGTC 2673
QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
    |||||||
Db 2674 CATTTCCACATACCACTATATTAATCTAGATTTTCTAGTGGGCTGGAAACCCATATGAT 2733
QY 841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
    |||||||
Db 2734 TTACAGATCATCTCTCGAGAGACACACATAGACTTCTGATGCGGAGAACATTAT 2793
QY 861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
    |||||||
Db 2794 GAATGTCATCTTTTGGACACTCACTTCCTCAAGAAACCTTGATCAGCATGATGCTCTAATA 2853
QY 881 ValIle 882
    |||||
Db 2854 GTGATA 2859

RESULT 4
AAD38956
ID AAD38956 standard; cDNA; 3120 BP.
XX
AC AAD38956;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human dipeptidyl peptidase 8 (DPP8) cDNA.
XX
KW Human: dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW antiviral; enzyme; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 214..2862
FT /*tag= a
FT /product= "Human DPP8 protein"
XX
PN MO200234900-A1.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001MO-AU01388.
XX

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PR 27-OCT-2000; 2000AU-0001078.
XX
PA (UNSY ) UNIV SYDNEY.
XX
PI Abbott CA, Gorrell MD.
XX
DR WPI: 2002-454646/48.
DR P-PSDB: AAE24170.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Example: Fig 1; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC sequence is human DPP8 cDNA.
XX
SQ Sequence 3120 BP; 936 A; 637 C; 706 G; 841 T; 0 other:
Alignment Scores:
Pred. No.: 0 Length: 3120
Score: 4700.00 Matches: 882
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-070-464-1 (1-882) x AAD38956 (1-3120)
QY 1 MetAlaAlaMetGluThrGlnLeuGlyValGluIlePheGluThrAlaSpCys 20
    |||||||
Db 214 ATGCACAGCAGCAATGGAACAGAACACTGGCTTGAGATTTGAAACGCGACGT 273
QY 21 GluLysAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
    |||||||
Db 274 GAGGAGAAATATTGAATACACAGATCGGCTTAATTTGAGCCTTTTATGTGACGGAT 333
QY 41 SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
    |||||||
Db 334 TCTGAGAGTCAAGCTTAAAGAGCTGCTTGCAGATCCAGAAATATCATGGCTACATGATG 393
QY 61 AlaLysAlaProHisAspPheMetCpheValLysArgAsnAspProAspGlyProHisSer 80
    |||||||
Db 394 GCTAAGGCACCAATGATTCATCTTTCTGAAAGCAATGATCCAGATGACATCATTTCA 453
QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
    |||||||
Db 454 GACAGAAATCTATTAACCTTGCCATGTGTGTAGAACAGAAATATACATCTTTTATTTCT 513
QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTyrLysProLeuLeu 120
    |||||||
Db 514 GAATTCGCCAAACTATCAATAGAGCAGCACTTATATGCTCTTGTGAACCTCTTTTG 573
QY 121 AspleuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
    |||||||
Db 574 GATCTTTTTCAGGCACACCTGGACTATGATGATTTCTCCAGAAAGAACTATTAGA 633
QY 141 GluArgLysArgIleGlyTyrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
    |||||||
Db 634 GAAGGAAACCATTTGGAACAGTGGAAATGCTTTTACAGATTTATCCACAGAGAGTGA 693
QY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
    |||||||
Db 694 ACATTTCTGTTCAAGCGGAGTGAATTTATCATCGTAAAGATGAGGCGCCAAAGGA 753
QY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
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Dh 754 TTTAGCCAAACCTTTAGGCCCAATCTAGTGGAAACCTAGTGTCCACATACGATG 813
Qy 201 Asprolylsleucysprolialaspasprospriprialeaiphellehisserasnaspiile 220
Dh 814 GATCCAAATTAATTCGCCCGATGATCCAGATGATGCTTTATATACATAGAACGATATT 873
Qy 221 TTPILeseraniilevaltharigluuargarqleuthrtyrvalhisasnigluu 240
Dh 874 TGGATATCTACATCGTATACAGAGAAAGAGAGACTCATTTATGTCCACATAGAGCTA 933
Qy 241 Alaasnmetgluualaspalaargseralaglyvalathrphervaluenglugu 260
Dh 934 GCCACACATGAG 993
Qy 261 Pheasparqyrseryltyrtriptpcysprolysaliagluuthrthprosergly 280
Dh 994 TTTGATAGATTTTCTGGCTATTGGTGGTGTCCAAAGCTGAAACACTCCAGTGGTGT 1053
Qy 281 Lysileleuargileleuargluuasnaspisusergluvalgluilehisval 300
Dh 1054 AAAATTTTACAGATTTATAGAGAAATGATGATGATGATGATGATGATGATGATGAT 1113
Qy 301 Thrserrprobleuugluuthrargaralaspserpheargtyrprolysthygthr 320
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Qy 321 Alaasnprolysalthrphelysmetsergluilemetileaspalagluvalargile 340
Dh 1174 GCAATCTTAAAGTACCTTTTAAAGATGTCAGAAATATGATGATGATGATGATGATG 1233
Qy 341 Ileaspyalileasplysgluileuileuinpropheliuleuphegluglyvalglu 360
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Qy 361 Tyrllealeaarglaglytrpthrprogluylgysrtyralatrpserileleuensp 380
Dh 1294 TATATGCGACAG 1353
Qy 381 Argsergintharargleuinilevalleuileserprogluileupheileprovalglu 400
Dh 1354 CGCTCCAGACTCGCGCTACAGATAGTGTGATCTCAGCTGATTTATTCAGGATAGA 1413
Qy 401 Aspspvalmetgluarggluargleuilegluservalproaspservalthrproleu 420
Dh 1414 GATGATGATGAG 1473
Qy 421 Ileleeryglugluuthrthaspriletrpilleasniilehisasprilephehisvalphe 440
Dh 1474 ATTATCTATGAG 1533
Qy 441 Proglinserrhisglugluilegluilepheleasergluucyslysthygthrlyphe 460
Dh 1534 CCCCAAGTCCAG 1593
Qy 461 Argthisleuylrlystlethserileleuysgluserlystlyllyllyllyllyl 480
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Qy 481 Glyleuprolalaproserasphelyscysprolielysgluuilealalilethrsr 500
Dh 1654 GGGCTGCTGCTCCAGAGATTTCAAGTGTCTTATCAAGAGAGATAGCAATTTCCAGT 1713
Qy 501 Glyleutrpgluvalleuarghisgluserasnileginalaspgluvalargarg 520
Dh 1714 GGTGAATGGAAGTTCTGGCGCGATGATGATGATGATGATGATGATGATGATGATG 1773
Qy 521 Leuvaltyrphlegluylthlyllyllyllyllyllyllyllyllyllyllyllyl 540
Dh 1774 CTGGTATATTTTGAAGCAGCAAGACCTCCCTTTAGAGACATCAGCTGATGATGATG 1833
Qy 541 Tyrtalaspnrogluyluvalthargleuthrhasparqlytyrserhissercyscys 560
Dh 1834 TACGTAAATCTGAG 1893

Qy 561 Ileserghisicysaspphepelleserlystlyserasnigluylasnasprohisicys 580
Dh 1894 ATCAGTACGACCTGTGACTTTTATAGTAGATATGTAAACGAGAGATCCACTGT 1953
Qy 581 Valserleuylrlyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 600
Dh 1954 GTGTCCCTTACAGATATCAAGTCTGAGATGATGATGATGATGATGATGATGATGAT 2013
Qy 601 TTPalathrileleuaspseralaglyproleuoproaspyrthrproprogluilephe 620
Dh 2014 TGGGCACACATTTGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2073
Qy 621 Serphegluserthrthgllypethrleuylrlyllyllyllyllyllyllyllyl 640
Dh 2074 TCTTTTGAAGTACTACTGATTTACATGATGATGATGATGATGATGATGATGATG 2133
Qy 641 GluProglyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 660
Dh 2134 CAGCTGGAAGAAATATCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2193
Qy 661 Valasnasnargpelysglyvallyllyllyllyllyllyllyllyllyllyllyl 680
Dh 2194 GTGATATATCGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2253
Qy 681 Tyrtalvalalileaspsnarqglysercysnarqglyleuyllyllyllyllyllyl 700
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Qy 701 AlaPhelystlyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 720
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Qy 721 Leuulaserargtyrasppheileaspleusparqvalglyllyllyllyllyllyl 740
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Dh 2434 GGAGATACCTCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2493
Qy 761 AlaGlyAlaProvalthleuThrleuThrpheThrsprthrglyllyllyllyllyl 780
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Qy 781 GlyHisProaspglnasnigluuileglttyrtyrleuuglyserValAlaMetGlna 800
Dh 2554 GGTCACTGACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2613
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Qy 821 HisPheAlaHisThrserileleuileuSerpheleuValargalaglyllyllyl 840
Dh 2674 CATTTTGACATACAGATATATCTGATGATGATGATGATGATGATGATGATGATG 2733
Qy 841 LeuGlnIleTytrProGlnIleArgHisSerIleatrgvalProgluserglyllyllyl 860
Dh 2734 TTACAGATCTATCTCAG 2793
Qy 861 GluLeuHisleuileuHislyllyllyllyllyllyllyllyllyllyllyllyllyl 880
Dh 2794 GAAGTCACTCTTTGACATCTTCAAGAAACCTTGATGATGATGATGATGATGATGAT 2853
Qy 881 ValIle 882
Dh 2854 GTGATA 2859
RESULT 5
AAH99934
ID AAH99934 standard; cDNA: 3143 BP.
XX

AAH99934:
 12-APR-2002 (first entry)
 cDNA encoding 21953 human prollyl oligopeptidase.
 21953 prollyl oligopeptidase; human; proline; endopeptidase;
 cancer; cardiovascular disease; autoimmune disease; atopic allergy;
 neuronal disorder; vascular disorder; prostate disorder; cytostatic;
 antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 diabetes mellitus; arthritis; multiple sclerosis; asthma;
 Grave's disease; neuronal disorder; demyelinating disease; ss.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 229..2877
 FT //tag=8
 FT /product="21953 prollyl oligopeptidase"
 FT /note="This region is specifically claimed in
 claim 2"
 WO200179473-A2.
 25-OCT-2001.
 11-APR-2001: 2001WO-US40483.
 18-APR-2000: 2000US-197508P.
 (MILL-) MILLENNIUM PHARM INC.
 Meyers RA, Williamson M;
 MPI: 2002-034353/04.
 P-PDB: AAC78415.
 New polypeptides 21953, member of human prollyl oligopeptidase family,
 useful as diagnostic targets and therapeutic agents for controlling
 cancer, lymphoma and leukemia
 Claim 7: Page 100-102: 121pp; English.
 This invention relates to an isolated 21953 human prollyl
 oligopeptidase, which is cytosolic, antidiabetic, antihypertensive,
 neuroprotective, antihypertensive, dermatological, antipsoriatic,
 antidiabetic, ophthalmological, antiinflammatory, nootropic,
 antiparkinsonian, anticonvulsant, gynaecological, vasorelaxant,
 antidiabetic, antidiabetic, antidiabetic, antidiabetic,
 antidiabetic in its action. Uses include gene therapy, expression or
 activity of 21953 protein modulator, it is useful for identifying a
 compound which binds to it and can be used in preventing, treating
 or detecting a cellular proliferative or differentiative disorder.
 The 21953 molecules can act as novel diagnostic targets and therapeutic
 agents for controlling disorders associated with the aberrant activity
 or degradation of peptide hormones e.g., disorders associated with cell
 differentiation and proliferation such as cancer, immune function,
 reproductive, neurological and cardiovascular function. The 21953
 molecules are thus useful for treating and preventing cellular
 proliferative and differentiative disorders, haematopoietic neoplastic
 disorders, immune disorders such as autoimmune diseases, diabetes
 mellitus, arthritis, multiple sclerosis, asthma, Grave's disease,
 neuronal disorders, demyelinating diseases, vascular disorders and
 CC metabolism or pain disorders. This sequence represents the cDNA
 encoding sequence of 21953 human prollyl oligopeptidase.
 SO Sequence 3143 BP; 943 A; 644 C; 712 G; 844 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3143
 Score: 4700.00 Matches: 882
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0
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QY 1 MetAlaAlaAlaMetGluThrGluGluGluGluValGluIlePheGluThrAlaAspCys 20			
DB 229 ATGCGACGACGACATGGAACAGAGACAGCTGGGTGTGAGATATTTGAAATCGGCGACTGT 288			
QY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheThrValGluArgTyr 40			
DB 289 GAGGAGAAATATGTAATCAGACGATGCGCTAAATGTGAGGCTTTTATGTGTGACCGGTAT 348			
QY 41 SerTrpSerGlnLeuLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60			
DB 349 TCCTGGAGTCAGCTTAAAGACGCTTCCGATACCGAAGAAATATCATGCTCATGATG 408			
QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80			
DB 409 GCTAAGGACACCATGATTTTCATGTTTGTGAAAGAAATATCATGATGACCTCATTTCA 468			
QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyLysAsnArgLysAsnArgLysPheTyrSer 100			
DB 469 GACAGATCTATTACCTTCCATGCTGTGAGAACAGAAATATACACTGTTTATTTCT 528			
QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120			
DB 529 GAAATTCGCAAACTATCATATAGACGACAGCTTAAATGCTCTTGGAAAGCCTCTTTTG 588			
QY 121 AspleuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgLysGluLysLeuArg 140			
DB 589 GATCTTTTTCAGGCAACACGACTGATGAAATGATTTCTGAGAAAGAAATATTAGAA 648			
QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrTrpAspTyrHisGlnGlySerGly 160			
DB 649 GAAAGAAACGATGTGACAGCTGGAATGCTTTTACCATTAATACCAAGAAAGTGA 708			
QY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180			
DB 709 ACATTTCTGTTTCAACCCGCTGATGCAATTTATCAGCTAAAGATGAGAGGCCAACAGCA 768			
QY 181 PheThrGlnGluProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200			
DB 769 TTTTACCACACACCTTTTAAAGGCCCAATCTGTGGAACCTAGTCCCAACATACGATG 828			
QY 201 AspProLysLeuGlyProAlaAspProAspTrpIleAlaPheLeuHisSerAsnAspIle 220			
DB 829 GATCCAAATATATGCTGCTGTGATCCAGACTGATGCTTTTATACATACCAACGATATT 888			
QY 221 TrpIleSerAsnIleValThrArgGluGluArgLysThrTyrValHisAsnGluLeu 240			
DB 889 TCGATATCTTACATCTGTAACACAGAGAAAGAGAGACTGCTTATGTGCAATGACCTTA 948			
QY 241 AlaAsnMetGluLysAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260			
DB 949 GCCAACATGTAAGAAATGTCACATGACGTCGATGCTCTTTGTTCACAAAGAA 1008			
QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280			
DB 1009 TTTGATGATATTTCTGCTATTTGTGTGTCACAAAGCTGAAACATCCACAGTGGTGT 1068			
QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGlySerGlyValGluIleIleHisVal 300			
DB 1069 AAATATCTTATGATTTCTATATGAAGAAATGATGATGAGTGGGAAATATATTCATGTT 1128			
QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320			
DB 1129 ACATCCCTATGTTGGAACACAGAGGCGCATTCCTTATCCCTAAACAGCTAC 1188			
QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspLysGluGlyArgGly 340			
DB 1189 GCAAATCTTAAGTCACTTTTAAAGATGTCAGAAATATGATGATGCTGAGAGAGGATC 1248			

QY 341 ILeaspValIleasPylsGluLeuIleGlnProPheGluIleLeuPheGluGluValGlu 360
 |||||
 Db 1249 ATGATGTCATAGATAGAGTAACTAATTCACCTTTTGATGATTTATTTGAAGGATTGAA 1308
 QY 361 TyrIleLeuArgAlaGlyTyrPheProGluGlyTyrAlaTyrPheIleLeuLeuAsp 380
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 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
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 Db 1369 CGCTCCAGACTGCCCGCAGATAGTGTGATCTCACCCTGATATTATTTCCAGTGA 1448
 QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
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 Db 1429 GATGATGTTATGGAAGAGCAGAGACTGATGAGTCACTGCTGATGCTGATCCACTA 1488
 QY 421 IleIleTyrGluGluTyrThrAspIleTyrIleAsnIleHisAspIlePheHisValPhe 440
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 Db 1489 ATATCTATGAGAAACAGACATCTGATTAATATCCATGACATCTTTCATGTTT 1548
 QY 1441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
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 QY 461 ArgHisLeuTyrLysIlePheSerIleLeuLysGluSerLysTyrLysArgSerGly 480
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 Db 1609 CGCTATTATACAAATTTACATCTATTTAAAGGAAAGCAATATTAACGATCCAGTGT 1668
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
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 Db 1669 GGGGTGCTGCTCCAAAGTATTCAGAGTCCATCAAGAGGAGATGCAATTAACAGT 1728
 QY 501 GlyLysIleProGluValLeuGluArgHisGlySerAsnIleGlnValAspGluValArg 520
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 Db 1729 GGTGAATGGGAAGTCTTGCGCGCATGAGATCAATATCCAAAGTGAATGAGTGAAGG 1788
 QY 521 LeuValTyrPheGluGluTyrThrLysAspSerProLeuGluHisIleLeuValValSer 540
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 Db 1789 CTGGTATATTTTGAAGGACCAAGACTCCCTTTAGAGCATCACCTGTAGCTAGTGTAGT 1848
 QY 541 TyrValAsnProGluGluValIleThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
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 Db 1849 TACCTAATCTCTGAGAGGTGACAGGCTGACTGACCTGCTGCTACATTTCTTGCTGC 1908
 QY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
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 Db 1909 ATCAGTCAGCACTGCTGACTCTTATAGTATAGTATGTAACAGAAATCCACACTGT 1968
 QY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
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 QY 601 TyrAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
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 QY 621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
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 QY 701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720

Db 2329 GCCTTAAATATAAATGGGTCAATATGAAATGACGATCAGGTGAGGACATCAATAT 2388
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 QY 741 GlyLysTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
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 Db 2449 GGAGGATACCTCTCCGATGGCATTAATGACAGAGTCAAGATATCTCTCAGGTTGCTATT 2508
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 Db 2569 GGTACCCCTGACAGATGACAGAGGCTATTACTTAGAGATCTGTGGCATGACAGCA 2628
 QY 801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
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 QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
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 Db 2689 CATTTGCACATACACGATATATTTACTGAGTGTGAGGCGTGGAAAGCCATATGAT 2748
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 Db 2869 GTGATA 2874
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 RESULT 6
 AAH99935 standard; cDNA; 2643 BP.
 ID AAH99935 standard; cDNA; 2643 BP.
 AC AAH99935;
 XX
 DT 12-APR-2002 (first entry)
 XX
 DE Coding sequence of 21953 human prolyl oligopeptidase.
 XX
 KW 21953 prolyl oligopeptidase; antibody; proline; endopeptidase;
 KW cancer; cardiovascular disease; autoimmune disease; atopic allergy;
 KW neuronal disorder; vascular disorder; prostate disorder; cytostatic;
 KW antidiabetic; antiarthritic; antiasthmatic; antiinflammatory;
 KW diabetes mellitus; arthritis; multiple sclerosis; asthma;
 KW Grave's disease; neuronal disorder; demyelinating disease; ss.
 KW
 OS Homo sapiens.
 OS
 PN NC0200179473-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 11-APR-2001; 2001MO-US040483.
 XX
 PR 18-APR-2000; 2000US-197508P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Meyers RA, Williamson M;
 XX
 DR WPI: 2002-034353/04.
 DR P-PSDB: AAG78415.
 XX


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Db 1501 GAATGGAGAGTCTTGGCCGCGCATGATCTAATATCCAACTGTGATGAGTCAGAGGCTG 1560
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QY 542 ValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysIle 561
Db 1621 GTAAATCCTGGAGAGGTGACAGAGCTGACCTGCTGCTACTACTACATTTCTGGTCATC 1680
QY 562 SerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCysVal 581
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QY 582 SerLeuTyrLysLeuSerSerProGluAspAspProThrLysLysThrLysGluPheTrp 601
Db 1741 TCCCTTTACAGCTATCAAGTCTGAGAGATGACCCAACTTCCAAACAAAGAAATTTGG 1800
QY 602 AlaThrIleLeuAspSerIleGlyProLeuProAspTyrThrProProGluIlePheSer 621
Db 1801 GCCACCAATTTGGATGAGCAGAGTCTCTCTCTGACTATATCTCCAGAAATTTCTCT 1860
QY 622 PheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeuGln 641
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QY 662 AsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGlyTyr 681
Db 1981 AATATCGCTTTAAGAGGATCAAGTAATTCGCTTGAATACCTTCAAGCTCTCTAGTTAT 2040
QY 682 ValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGlyVal 701
Db 2041 GTGGTTAGTAGTAGACAAACAGGGGATCCTGACCCAGGGCTTAAATTTGAAGGCCCC 2100
QY 702 PheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlyTyrLeu 721
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QY 782 HisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGluLys 801
Db 2341 CACCTTACACAGATGAAAGGCTTATTAAGTATGATCTGGCCATGACAGCAAGAAAG 2400
QY 802 PheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGluAsnValHis 821
Db 2401 TTTCCCTCTGAACCAATTCGTTTACTGCTCTTACATGGTTCCCGATGGAAGATGTCAT 2460
QY 822 PheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAspLeu 841
Db 2461 TTTTGCATATACCACTATATTAAGTATTTTATGAGGGCTGGAAGCCATATGATTTA 2520
QY 842 GlnIleTyrProGluGluArgHisSerIleArgValProGluSerGlyGluHisTyrGlu 861
Db 2521 CAGATCTATCTCTGAGAGACACAGACATAGAGTCTCTGAAATCGGGAACATTAAGAA 2580
QY 862 LeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaIleLeuLysVal 881
Db 2581 CTGCATCTTTTGCACCTTCAAGAAACCTTGATCAGTATTTGCTGTCTTAAAGTG 2640

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QY 882 Ile 882
Db 2641 ATA 2643

RESULT 7
ID ABR83327 standard; cDNA: 4829 BP.
XX
AC ABR83327;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPP-1 splice variant #3.
XX
KW Human: serine protease; dipeptidyl peptidase IV-related protein; DPP;
KW DPP-IV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinnesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN M0200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001MO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR ) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junten J;
XX
DR WPI: 2002-444178/47.
XX
PT P-PSDB; ABR61596.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
XX
PS Disclosure: Page 65-66; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
CC proteins (DPP-IV). The dipeptidyl peptidase IV-related proteins (DPP-IV)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinnesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABR83327-ABR83343 encode human DPP-IV proteins.
XX
SQ Sequence 4829 BP; 1466 A; 886 C; 1017 G; 1460 T; 0 other;
XX
Alignment Scores:
Pred. No.: 0 Length: 4829
Score: 4680.00 Matches: 882
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.57% Indels: 2
DB: 24 Gaps: 0

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US-10-070-464-1 (1-882) x ABR83327 (1-4829)

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OY	21	GIuGIuAsnIleGluSerGlnAspArgProIysIleuGluProPheTyrValGluIuArgTyr	40
Db	274	GAGGAGATATTGAATACAGAGATCGGCTTAATTGGAGCCCTTTTATTGTTCAGCGGAT	333
OY	41	SerTrpSerGlnIleuLysLysIleuAlaAspThrArgLysTyrHisGlyTyrMetMet	60
Db	334	TCTCGAGTAGTACGCTTAAAGAGCTGTGGCCGATACAGAAATATCATGCTACATGTATG	393
OY	61	AlaLysAlaProHisAspPheMetIleValIArgAsnAspProAspIyProHisSer	80
Db	394	GCTAAGGACCAACATGATTTATCATGTTGTGAAGAAATGATTCACATGAGCTCATATCA	453
OY	81	AspArgIleTyrTyrIleuAlaIaMetSerGlyGlnAsnArgIuAsnThrPhePheTyrSer	100
Db	454	GACGAAATCTATACCTTACCTTGGCATGTGGTGAGAACAGAAATACACTGTTTATTCT	513
OY	101	GluIleProIysThrIleAsnArgAlaAlaValIleuMetLeuSerTrpLysProIleuLeu	120
Db	514	GAAATTCCTCCAAATATCAATATAGCAGCAGCTTATGCTCTCTTGGAAAGCCCTATTGG	573
OY	121	AspLeuPheGlnAlaThrIleAsnAspTyrGlyMetTyrSerArgGluGluIleuLeuArg	140
Db	574	GATCTTTTTCAGGCAACACCTGGACATGAGATGATTATTCGAGACAGAACACTATTAA	633
OY	141	GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnIysGly	160
Db	634	GAAAGAAACCATTTGGAGACAGCTGGCAATGCTTTCAGATGATATCCACAGAAAGTGA	693
OY	161	ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyLysProGlnGly	180
Db	694	ACATTTCTGTTTCAAGCCGGAGGGAGATTATACAGTAAAGATGAGAGGCCACAGGA	753
OY	181	PheThrGlnGlnProLeuArgProAsnIleuValGluThrSerCysProAsnIleArgMet	200
Db	754	TTTACGCAACACCTTTAAGGCCCAATCTAGTGGAACTAGTTGTCCAACTACGAGATG	813
OY	201	AspProIysIleuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle	220
Db	814	GATCCAAATATTAATGCTCTGCTGATCCAGACTGGATGGATTTGTTTATACATGCAACATAT	873
OY	221	TrpIleSerAsnIleValIThrArgGluLysArgLysIleThrTyrValHisGlnIleu	240
Db	874	TGGATATCTAATCATCGTAACACAGAAAGAAAGAGACTCACTTATGTGCACATATGCTA	933
OY	241	AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaIaThrPheValIleuGlnIleu	260
Db	934	GCCACACATGGAAAGATGCCACATCCAGCTGGAGTGGCTACCTTTGTTCTCCAAAGAGA	993
OY	261	PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly	280
Db	994	TTTGATATGATATCTGTGCTATGTGGTGTGTGCCAAAAGCTGAAACACTCCCGAGTGGT	1053
OY	281	LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal	300
Db	1054	AAATTTCTTGAATTTCTATATGAAAGAAATGATGATTCGAGGTGGAATTTATTCATGTT	1113
OY	301	ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrTrpProLysThrGlyThr	320
Db	1114	ACATCTCCCTATGTTGGAAACAGAGGGCAGATTCAATCCGTTATCTCTAAACAGGTACA	1173
OY	321	AlaAsnProLysValIThrPheLysMetSerGluIleMetIleAspAlaGluLysArgIle	340
Db	1174	GCAATCTCTAAAGTCACTTTTAAGATGTGAGAAATATATGATTTGATCTGAAGAGAGATC	1233
OY	341	IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluIleValGlu	360
Db	1234	ATAGATGTGCATAGTAAGAACTAATTCACCTTTTGAGATTTCTATTATTGAAGAGTGTGA	1293

QY	361	TYRILEAIAAGIAGLYTPRTHRPROGLUGLYSGTYAIAIRPSETRIELEUENASP	380
Db	1294	TATATTTGGCAACAGCTGGATGGACTCCTCGAAGGAAATATGCTTGGTCATCCTACTACAT	1353
QY	381	ARGSERGINTHRAAGLEAGINILEVALLEULESERPROGLEUPHELLEPROVALGLU	400
Db	1354	CGCTTCCAGACTCCCTCTACAGATAGTGTGATCTCACCTGAATTATTTATCCCACTACAA	1413
QY	401	ASPAVALMEICLUARGINARGLEULEGLUSERVALPROASPERVALTHPROLEU	420
Db	1414	GATGATGTTATGGAAGGACAGACATCATTTAGCTAGCTGCTGATATCTGTGACGCCACTA	1473
QY	421	ILEILETYRGLUGLUTHRTHRASPILLETPRIEASNILEIASPILLEHISVALPHE	440
Db	1474	ATTATCTATGTAAGAAACACAGACATCTGGATAAATATCCATCAGCATCTTTCATCTTTT	1533
QY	441	PROGINSERHISGLUGLUGLILEGLUPHEILEPHALSERGLUCYSYSTRHGLYPHE	460
Db	1534	CCCCAACTCCGAGAGGAAATTTGATTTATTTTGGCTCTGATGACAAACAGGTTTC	1593
QY	461	ARGHISLEUYYRLYSILETHRSERILELEULYSGLUSERLYSTRYSARGSERGLY	480
Db	1594	CGTCAATTTATACAAATTTACATCTATTTTAAAGAAACCAATATTAACGATCCAGTGST	1655
QY	481	GLYLEUPROALAPROSERASPHELYSCYSPROILEYSGLUGLUILEALILETHRSER	500
Db	1654	GGGCGCTCTCTCCCAAGTGTCAATGCTTCATCAAGAGAGAGATACCATTTACCACT	1713
QY	501	GLYGLUTPRGLUVALILEUGLYARGHISGLYSERASNILEGLIVALASPOLVALARGAR	520
Db	1714	GCTGAATGGGAAGTCTTGGCCGGCATGATCTAAATATCCAGTTGATGTAAGTCAAGAG	1773
QY	521	LEUVALTYRPHIEGLUGLYTHRILYSPSPSERPROLEGLUHISHISLEUVALVALSER	540
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QY	541	TYRVALASNPROGLUGLUNALTHRARGLEUTHRASPARGLYTRISERHISISERCYCS	560
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QY	561	ILESERGINHISCYSPASPHEPHEILESERLYSTRISERASNGLNASNPROIHISCY	580
Db	1894	ATCATCTAGCACTGTGACTCTTTATTAAGTAATATAGAACAGAGAAATCCACACGT	1953
QY	581	VALSERLEUYYRLYSLEUSERSERPROGLIASPAPPROTHCYSLYSTRHYSGLUPHE	600
Db	1954	GTGTGCTCTTACAGGCTATCATCAAGTCCCTGAAGATGACCACCACTTGCAGAAACGAATTT	2013
QY	601	TRPALATHRIELEUASPERALAGLYPROLEUPROASPTYRTHRPROBROGLUILEPHE	620
Db	2014	TGGGCACCATTTTGGATTCAGCAGGTCCTCTTCGAGATATACCTCCACAGAAATTTTTC	2073
QY	621	SERPHIEGLUSERTHRTHRGLYPHERHLEUTHYGLYMELEUTHYRILYSPROIHISAPLEU	640
Db	2074	TCTTTTGAATCTACTGTGATTTTACCTTGTATGAGATCCTCTACAAAGCTCATATATCTA	2133
QY	641	GLNPROGLYLSYSTRYPROTHRVALLEUPHEILETYRGLIGLY--PROGINVALINL	660
Db	2134	CAGCTTGGAAGAAATCTCTACTGTGCTCTTATATATGCTGCTCTCTCCACGGTGCAGT	2193
QY	660	EUVALASNPASPARGPHELYSGLYVALYSTYRPHEARGLYEUASNTHRIEUALASERLEAG	680
Db	2194	TGTGTAAATATCGGTTTAAAGAGATCAAGATTTCCGGCTTGAAATACCCAGCTCTCTAG	2253
QY	680	LYTYRVALVALVALILEASPARAGLYSERCYSHISARGILEULYSPHIEGLUC	700
Db	2254	GTTATGTGGTGTGTGATGATAGACACAGGGGATCTCTGACCGAGGGCTTTAAATTTTGAAG	2313
QY	700	LYALAPHELYSTRYLYSMEGLVGLINILEGLUILEASPARGINVALIGLUGLYLEAGINT	720
Db	2314	GGGCTTTAAATATTAATATGGGTCAAAATTAACAATACATCAGGGGAGAGACTCCCAAT	2373
QY	720	YRLEUALASERARGTYRASPHEILESPHEUNSPARVALGLYLEHISGLYTPRSET	740

Db 814 GATCCAAATTATGCGCTGCTGATCCAGACTGGATTGCTTTTATACATGACAGCATATT 873
 QY 221 TTPILeserAinileValjThrArgGluGluArgArgLeuThrTyValHisasnGluLeu 240
 Db 874 TGGATATCTAACATCGTACGACAGAGAAAGAGACGCTACTATGTCACATAGCTA 933
 QY 241 AAlasmetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260
 Db 934 GCCAACATGAGAGAGAGATGCCAGATCAGCTGAGTGGCTACTCTTGTCTCCAAAGAA 993
 QY 261 PheAspArgTySerGlyTyTrpTrpCysProLysAlaGluThrThrProSerGly 280
 Db 994 TTTGATGATATTTCTGGCTATTGGTGTGTCACAAAGCTGAAGACACTCCAGTGGT 1053
 QY 281 LysIleLeuArgIleLeuTyGluGluAsnAspGluSerGluValGluIleIleHisVal 300
 Db 1054 AAAATTTCTAGAAATCTATATGAGAAATGTAATCTGAGGTGGAATTTATCATGTT 1113
 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyTrpProLysThrGlyThr 320
 Db 1114 ACATCCCTATGTTGGAAACAGAGGCGACATTCATTCCTGTTATCTTAAACAGCTACA 1173
 QY 321 AAlasProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
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 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 Db 1234 ATAGATGTCATAGATAAGAACTAATTCACCTTTTGATTTGATTTGAAGAACTTGA 1293
 QY 361 TyrIleAlaArgIleGlyTrpThrProGluGlyLysTyTrpAlaTrpSerIleLeuLeuAsp 380
 Db 1294 TATATTCGCAAGCTGGATGTGACCTCTGAGGAAATATGCTGTGCTCATCTCATAGAT 1353
 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProAlaGlu 400
 Db 1354 CGCTCCAGACTCCGCTACATAGATGTGATCTCACCCTGAATTTATATCCCACTAGA 1413
 QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
 Db 1414 GATGATGTTATGAAAGGACAGACTCATGTGATGATGCGCTGATGCTGACGCGCACTA 1473
 QY 421 IleIleTyGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
 Db 1474 ATTATCTATGAGAAACACAGACATCTGGATTAATATCATGACATCTTTCACTGTTT 1533
 QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
 Db 1534 CCCCAAGTCCAGAGAGAGAAATGAGTTTATTTTGGCTCTGAATGCAAAACAGGTTTC 1593
 QY 461 ArgHisLeuTyTrpLysIleThrSerIleLeuLysGluSerLysTyTrpLysArgSerGly 480
 Db 1594 CGTCATTTATACAAATATACATATTTTAAAGAAACCAATATAACGATCCAGTGGT 1653
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
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 QY 501 GlyLysTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
 Db 1714 GGTGAATGGGAAGTCTTGGCGCGCATGATCTAATATCCAAAGTTGATGAAGTCCGAAGG 1773
 QY 521 LeuValTyTrpPheGluGlyThrLysAspSerProLeuGlnHisIleLeuTyValValSer 540
 Db 1774 CTGGATATTTTGAAGGACCAAGACATCCCTTAGAGCATACCTGTAGCTAGTACTAGT 1833
 QY 541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyTrpSerHisSerCys 560
 Db 1834 TACGTAATCTCTGGAGAGTACAGAGCTGACTGACCTGGCTACTCTCACTTCTTGGC 1893
 QY 561 IleSerGlnHisCysAspPheIleSerLysTyTrpSerAsnGluLysAspProHisCys 580
 Db 1894 ATCAGTCCGACACTGTGACTTTTATATAGTATAGTAAACCAAGAAATCCACACTGT 1953

QY 581 ValSerLeuTyTrpLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
 Db 1954 GTCTCCCTTTACAACTATTCAAAGTCTCTGAGATGACCCCACTGTGCAAAACAAAGCAATT 2013
 QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyTrpProProGluIlePhe 620
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 QY 621 SerPheGluSerThrThrGlyPheThrLeuTyTrpGlyMetLeuTyTrpLysProHisAspLeu 640
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 QY 641 GlnProGlyLysTyTrpProThrValLeuPheIleTyGlyGlyProGlnValGlnLeu 660
 Db 2037 -----CCTCAGGTGCAAGTTG 2051
 QY 661 ValAsnAsnArgPheLysGlyValLysTyTrpPheArgLeuAsnThrLeuAlaSerLeuGly 680
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 QY 681 TyrValValAlaValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
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 QY 701 AlaPheLysTyTrpLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyTrp 720
 Db 2172 GCCTTTAATATATAATATGGTCAATATGACAAATTTGACAGTGGAGACTCCCAATAT 2231
 QY 721 LeuAlaSerArgTyTrpAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerTyTrp 740
 Db 2232 CTAGCTTCTCGATATGATGATTTCACTTACATGATCTGTGGCGCATCCAGCGCTGCTCAT 2291
 QY 741 GlyLysTyTrpLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
 Db 2292 GGAGGATACCTCTCCCTGATGGCATTAATGACAGAGTCAAGATATCTTCAGGTTCTCAT 2351
 QY 761 AlaGlyAlaProValThrLeuTrpIlePheTyTrpAspThrGlyTyTrpGluArgTyTrpMet 780
 Db 2352 GCTGGGGCCCGACGTCAGTCTGTGATCTTTATGATACAGATACAGGAAAGCTTATATG 2411
 QY 781 GlyHisProAspGlnAsnGluGlnGlyTyTrpLeuGlySerValAlaMetGlnAlaGlu 800
 Db 2412 GGTCACTCCCTGACAGAAATGAAACAGGCTTATCTAGGATCTGTGGCCATGCAACAGAA 2471
 QY 801 LysPheProSerGluProAsnArgLeuLeuLeuHisGlyPheLeuAspGluAsnVal 820
 Db 2472 AGGTTCCTCTGAACCAAAATGTTTACTGCTTACATAGGTTTCTGGATGAGATGCTC 2531
 QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysArgTyTrpAsp 840
 Db 2532 CATTTTGCATACACAGATATATCTAGTGTTTTATGAGAGGGCTGGAAAGCATATGAT 2591
 QY 841 LeuGlnIleTyTrpProGlnGluArgHisSerIleArgValProGluSerGlyGlnHisTyTrp 860
 Db 2592 TTACAGATCTATCCCTCAGAGAGACACAGACATAAAGTTCCTGAATCCGGAGAACATTA 2651
 QY 861 GlyLeuHisIleLeuHisIleTyTrpLeuGlnGluAsnLeuGlySerArgIleAlaAlaLeuLys 880
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 QY 881 ValIle 882
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 ABRK8331
 ID ABRK8331 standard; cDNA: 4676 BP.
 AC ABRK8331:
 XX
 .DT 12-AUG-2002 (first entry)
 XX

DE cDNA encoding human DPRP-1 splice variant #7.
 XX
 XX Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX
 PA (FERR) FERRING BV.
 XX
 PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
 DR WPI: 2002-444178/47.
 DR P-PSDB: AB661600.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT .
 XX
 PS Disclosure: Page 72-73; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychophoric and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABR83322-ABR83343 encode human DPRP proteins.
 CC
 XX
 SQ Sequence 4676 BP; 1424 A; 859 C; 979 G; 1414 T; 0 other;
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 Alignment Scores:
 Pred. No.: 0 Length: 4676
 Score: 4385.00 Matches: 831
 Percent Similarity: 94.22% Conservative: 0
 Best Local Similarity: 94.22% Mismatches: 1
 Query Match: 93.30% Indels: 51
 DB: 24 Gaps: 1
 US-10-070-464-1 (1-882) x ABR83331 (1-4676)
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 QY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
 DB 274 GAGGAAATATTCATCAACAGATCGGCTAAATTTGAGAGCTTTTATGTTGAGCGGTAT 333
 QY 41 SerTyrSerGlnLeuTyrLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 DB 334 TCTTGAGTACGCTTAAAAAGCTGCTTGGCGATACCAAGAAATATATCATGCTACATGATG 393

QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspLysProHisSer 80
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 QY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspLysGlyProGlnGly 180
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 QY 361 TyrIleAlaArgAlaGlyTyrThrProGluGlyLysTyrAlaTyrSerIleLeuLeuAsp 380
 DB 1294 TATATTTGCCAGACTGATGAGACTCTTGAGGGAATATGCTTGCCATCTACTAGAT 1353
 QY 381 ArgSerGlnThrArgLeuGlnIleValIleSerProGluLeuPheIleProValGlu 400
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 QY 401 AspAspValMetGluArgGlnArgGluIleGluSerValProAspSerValThrProLeu 420
 DB 1414 GATGATGTTATGGAAGGACGACATCATTTGACTGCTGCTGATCTGTGAGCCACACTA 1473
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Alignment Scores:

Pred. No.:	0	Length:	2842
Score:	4118.00	Matches:	782
Percent Similarity:	88.66%	Conservative:	0
Best Local Similarity:	88.66%	Mismatches:	100
Query Match:	87.62%	Indels:	1
DB:	24	Gaps:	1

US-10-070-464-1 (1-882) x ABNS9774 (1-2842)

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OY 1 MetAlaAlaMetGluThrGluGlnLeuGlyAlaGluIlePheGluThrAlaAspCys 20
DB 234 ATGGCACACCAATGAAAGAAAGAACACCTGGCTGTGATATTGAAACGCGACTGT 293
OY 21 GluGlnAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrlValGluArgTyr 40
DB 294 GAGGAGAAATTTGATACAGGATCGGCTTAATGGAGCCCTTTTATGTTGACGGGTAT 353
OY 41 SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
DB 354 TCCGTGAGTCAGCTTAAAGAGCTCTGGCGATCCAGAAATATCATGGCTACATGATG 413
OY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
DB 414 GCTAAGGACCCACATGATTTTCATGTTGTGAAGAGAAATGATCCAGATGGACCTCATTC 473
OY 81 AspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGluAsnThrLeuPheTyrSer 100
DB 474 GACAGATCTATTTACTCTCCATCTCTGTCGAGACAGAGAAATACACTGTTTATCTT 533
OY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTyrPlysProLeuLeu 120
DB 534 GAATTTCCCAAACTATCATATAGACGACAGCTTAAATGCTCTCTGGAAGCCCTTTTG 593
OY 121 AspleuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
DB 594 GATCTTTTTCAGCACACGAGCTAGTAAATGATTTCTCGAAGAAAGAACTATTAAGA 653
OY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnIleSerGly 160
DB 654 GAAGAAGAAACCATTTGAGACAGCTCGAATTCCTTTACATTTTCACCAAGAAAGTGA 713
OY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
DB 714 ACATTTCTGTTTCAAGCCGAGTGAATTAATCACCCTAAAGATGAGGGCCCAAGA 773
OY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
DB 774 TTTCAGCACACCTTTAAGGCCCAATCTAGTGAACCTAGTGTCCCAACATACGGATG 833
OY 201 AspProLysLeuCysProAlaAspProAspTyrIleAlaPheIleHisSerAsnAspIle 220
DB 834 GATCCAAATATTATGCTCGTGCATCCAGACGATGCTGTTTATATACATAGCAACATATT 893
OY 221 TrpIleSerAsnIleValIleThrArgGluGluArgLysLeuThrTyrValHisAsnGluLeu 240
DB 894 TGGTATCTTAACATCTTAACAGAGAAAGAAAGAGACTCATTTATGTCACAAATGACTA 953
OY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260
DB 954 GCCAACATGGAAGAGATGCCAGATCAGCTGAGTCCCTGTTGTTCTCCAGAAAGAA 1013
OY 261 PheAspArgTyrSerGlyTyrTyrTrpCysProLysAlaGluThrThrProSerGlyGly 280
DB 1014 TTTCATGATGATATTCTGCTATTTGCTGTGCCAAAGCTGAACAACTCCAGAGTGGGT 1073
OY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
DB 1074 AAAATTTCTGAATTTCTATATGAAGAAATGATGAATCTGAGTGGAAATATTCATGTT 1133
OY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
DB 1133

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DB 1134 ACATCCCTATGTTGAAACAGAGCGAGATTTCCTCCGTTATCCCTAAACAGCTACA 1193
OY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluArgIle 340
DB 1194 GCAAATCCCTAAAGTCACTTTTAAAGATCTGAAATATATGTTATGCTGAGAGAGATC 1253
OY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
DB 1254 ATGATGCTATGATAGTAAGAACTAATCAACCTTTTGAATCTCATTTGAAGAGTTGAA 1313
OY 361 TyrIleAlaArgAlaGlyTyrThrProGluGlyLysTyrThrAlaPheSerIleLeuLeuAsp 380
DB 1314 TATATTGCCAGAGCTGGATGAGTCCCTGAGGAAATATGCTTGCTCATCTACTAGAT 1373
OY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
DB 1374 CGCTCCAGACTGCGCTACAGATATGTTATCTCACCCTGAATTTATCCAGTGA 1433
OY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
DB 1434 GATGATGTTATGAAAGCGAGAGACTCATTCAGTCACTGCTGATTCGTGAGCGCCACTA 1493
OY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
DB 1494 ATTATCTATGAGAAACACAGACATCTGATTAATATCCATGACATCTTTCATGTTTTT 1553
OY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
DB 1554 CCCCAAGTCCAGAGAGAAAGAAATGATTTATTTTCCCTGATTCGAAACAGGTTTC 1613
OY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
DB 1614 CGTCATTTATACAAATTAATCATTTTAAAGCAAGCAAAATTAACATCCAGTGT 1673
OY 481 GlyLeuProLapProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
DB 1674 GGGCTGCTGCTCCAAAGTCAATTTCAAGTCTCTCAAGAGAGATAGCAATTTACCAGT 1733
OY 501 GlyLeuTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
DB 1734 GGTAAATGGAGAGTCTTGGCGGCGCATGATCTAATATCCAGTGAATGAGTGAAGG 1793
OY 521 LeuValTyrPheGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValIleSer 540
DB 1794 CTGGTATATTTTGAAGGACCAACAAAGCTCCCTTAAAGCATCACCTGTACGTAGT 1853
OY 541 TyrValAsnProGluGlyValIleThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
DB 1854 TACGTAAATCTCGAGAGCGTACAGAGCTGACCTGACCTGCTACATCTTCTGCTGC 1913
OY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGlnLysAsnProHisCys 580
DB 1914 ATCAGTCAGACAGCTGACTCTTTATTAAGTAAGTAAGTAACAGAGAAATCCACACTGT 1973
OY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
DB 1974 GTGGCCCTTTAACAAGCTATCAAGCTCGAAGATACCCCACTTGCACAAAGAAATTT 2033
OY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
DB 2034 TGGGCCACCATTTTGGATTAGACAGGCTCTTCTTACTACTACTCTCCAGAAATTTTC 2093
OY 621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
DB 2094 TCTTTTAAAGTACTACTGATTTACATTTGAATGGATGCTTCAAGCCCTCAGATCTA 2153
OY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
DB 2154 CAGCTTGAAAGAAATATCTTACTGCTGCTCATATATATGATGCTGCTCCTCAG 2204
OY 661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
DB 2204 ----- 2204

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Db 2550 GTGATA 2555

RESULT 12

AAD23843

ID AAD23843 standard; cDNA: 2510 BP.

XX AAD23843;

AC

XX

DT 07-MAR-2002 (first entry)

XX

DE Human protease PRTS-2 cDNA.

XX

XX Human; protease: PRTS-2; tranquilizer; gene therapy; vaccine; allergy; infection; dermatitis; arteriosclerosis; rheumatoid arthritis; hepatitis; atherosclerosis; psoriasis; Alzheimer's disease; mental disorder; cancer; gastrointestinal disorder; Cushing's syndrome; seizure; glaucoma; stroke; epithelial disorder; urticaria; anorexia; trauma; asthma; eczema; nausea; hypertension; neurological disorder; Parkinson's disease; drug screening; candida; cell proliferative disorder; multiple sclerosis; osteoporosis; diabetes mellitus; glomerulonephritis; cardiovascular disorder; anaemia; autoimmune disorder; inflammatory disorder; myocardial infarction; AIDS; developmental disorder; reproductive disorder; infertility; diarrhoea; dementia; acidosis; cataract; gynaecomastia; epilepsy; jaundice; ss.

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT CDS 616..2358

FT /Product= "Human protease PRTS-2 protein"

PN MO200183775-A2.

XX

XX 08-NOV-2001.

XX

XX 04-MAY-2001: 2001WO-US14651.

XX

XX 04-MAY-2000: 2000US-202082P.

PR 11-MAY-2000: 2000US-203566P.

PR 17-MAY-2000: 2000US-205803P.

PR 25-MAY-2000: 2000US-207477P.

PR 01-JUN-2000: 2000US-209402P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Deleage AM, Lal P, Hafalia A, Patterson C, Walla NK, Kearney L; Tribouley CM, Khan FA, Yao MG, Baughn MR, Azimzai Y, Elliott VS; Nguyen DB, Gandhi AR, Yang J, Hernandez R, Policky JL, Lu DM; Reddy R, Yue H, Tang YT;

XX

DR MPI: 2002-034518/04.

XX

XX P-PSDB: AAE14337.

PT Novel human proteases and polynucleotides encoding the proteases, useful for treating, diagnosing or preventing cell proliferative, cardiovascular, autoimmune/inflammatory, neurological and developmental disorders -

PT

XX

PS Claim 5: Page 139-140; 151pp: English.

XX

XX The invention relates to human proteases (PRTS-14) and its corresponding cDNA molecules. Human PRTS and its nucleic acid molecule are useful for the diagnosis, treatment and prevention of disorders associated with increased or decreased expression of PRTS. Examples of such disorders include, cell proliferative disorders (arteriosclerosis, atherosclerosis, hepatitis, psoriasis and cancers); autoimmune/inflammatory disorders (AIDS, Addison's disease and cancers); asthma, atopic dermatitis, diabetes mellitus, glomerulonephritis, multiple sclerosis, osteoporosis, trauma, Grave's disease, rheumatoid arthritis, ulcerative colitis, and viral, bacterial, fungal, parasitic, protozoal and helminthic infections); cardiovascular disorders (myocardial infarction, ischaemic heart disease and hypertension); neurological disorders (epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, dementia,

CC Parkinson's disease, stroke, mental disorders including mood, anxiety CC and seasonal affective disorder and prion diseases); gastrointestinal disorders (Crohn's disease, anorexia, nausea, diarrhoea and jaundice); CC epithelial disorders (contact dermatitis, eczema, acne vulgaris, CC alopecia, scabies, insect bites and urticaria); reproductive disorder CC (infertility, disruption of estrous and menstrual cycle and CC gynaecomastia); and developmental disorders (renal tubular acidosis, CC Cushing's syndrome, seizure disorders, congenital glaucoma and cataract). CC PRTS DNA is also in useful is gene therapy. PRTS and its immunogenic CC fragments are useful for screening libraries of compounds in several drug CC screening assays. The present sequence is human protease PRTS-2 cDNA. CC

XX

SO Sequence 2510 BP; 777 A; 494 C; 527 G; 712 T; 0 other;

XX

Alignment Scores:

Pred. No: 0 Length: 2510

Score: 3970.50 Matches: 764

Percent Similarity: 89.81% Conservative: 3

Best Local Similarity: 89.46% Mismatches: 5

Query Match: 84.48% Indels: 82

DB: 24 Gaps: 6

US-10-070-464-1 (1-882) x AAD23843 (1-2510)

Oy 42 TTPserGlnLeuLysLysLeuAlaAspThrArgLysTrpHisGlyTrpMetCeta 61

Db 3 TGGAGTCAGCTTAAAGAGCTGCTGGCGATACCGAAATATCTCGCTACATATGCT 62

Oy 62 LysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSerAsp 81

Db 63 AAGCACCACATGATTTTCATGTTGTGAAGAGAAATGATCAGATGACCTATTTCAGAC 122

Oy 82 ArgLysTrpTrpLeuAlaMetSerGlyGluAsnArgGluAsnTrpLeuPheTrpSerGlu 101

Db 123 AGAATCTATTACCTTGGCATGTGTGAGAACAGAAATACATGTTTTATTCTGAA 182

Oy 102 ILeuProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeuAsp 121

Db 183 ATTCCCAAAACTATCATATAGACGACGCTTTAATGCTCTTGGAAAGCCCTTTTGAT 242

Oy 122 LeuPheGlnAlaThrLeuAspTrpGlyMetTrpSerArgGluGluLeuLeuArgGlu 141

Db 243 CTTTTCAGCAACACATGAGCATATGAAATGATTCGAGAAAGAAATTTAAGAA 302

Oy 142 ArgLysArgIleGlyThrValGlyIleAlaSerTrpAspTrpHisGlnGlySerGlyThr 161

Db 303 AGAAACGCAATGGAGACAGTCGAAATTCCTTACATATATACCAAGAAAGTGACAA 362

Oy 162 PheLeuPheGlnAlaGlySerGlyIleTrpHisValLysAspGlyGlyProGlnGlyPhe 181

Db 363 TTTCTGTTTCAAGCCGCTAGTGAATTTATTCACCTAAAGATGAGGCGCAAGGATTT 422

Oy 182 ThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAsp 201

Db 423 ACCGAAACACTTTAAAGCCCAATCTAGTGAAGCTAGTTGTCACCAATACGATGAT 482

Oy 202 ProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIleTrp 221

Db 483 CCAAAATTAATGCCCTGCTGATCCAGACTGATTCCTTTTATACATACCAAGATATTTGG 542

Oy 222 ILeuSerAsnIleValIThrArgGluGluIArgArgLeuThrTrpValHisAsnGluLeuVal 241

Db 543 ATATCTTACATCTGTAACACAGAGAAAGAAAGAGACTCATTTATGTGCCAATGAGCTAGCC 602

Oy 242 AsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPhe 261

Db 603 AACATGGAAGAGATGCGACATGAGTGCAGTGCCTGCTTTGTTCCAAAGAAAGATTT 662

Oy 262 AspArgGlySerGlyTrpTrpTrpCysProLysAlaGluThrTrpProSerGlyGlyLys 281

Db 663 GATGATATATCTGCGCTTGTGTGTGTGTCCAAACCTGAACACTCCCATGTGTGCTAAA 722

Oy 282 ILeuLeuArgIleLeuValTrpGluGluAsnAspCysLeuValGluIleIleHisValThr 301

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Db 723 ATTCTGAAATCTATATGAAAGAAATGATCAATCTGAGTGGAATATTTCAGTTACA 782
Oy 302 SerProMetLeuGluThrArg-ArgAlaAspSerPheArgTyrProLysThrGlyThrAl 321
Db 783 TCCTCTATGTTGGAAACAGGACGAGATTCATCCGTTATCCTTAAACAGGACGAC 842
Oy 321 aasnProLysValThrPheLysMetSerGluLeuMetIleAspAlaGluArgIleI 341
Db 843 AAATCTTAAAGTCACTTTAAGATGTGCAAAATATATGATTCATGCTGAAGAGAGATCAT 902
Oy 341 easpValIleaspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGluTyr 361
Db 903 AGAGTCTATAGATAGGAACTCAATTCACCTTTGAGATTCATTTTGAAGAGATTGAATA 962
Oy 361 rIleAlaIArgAlaGlyTThrPThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAspAr 381
Db 963 TATTGCCAGACTGGATGAGATCCTCGAGGAAATATGCTTGCTCCTACTACTAGATCG 1022
Oy 381 gSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGluAs 401
Db 1203 CTCCAGACGCTGCTACAGATAGTGTGATCTCAGCTCAATTAATTTATCCAGTAGAGA 1082
Oy 401 pasPValMetLuarGlnArgLeuIleGluSerValProAspSerValThrProLeuI 421
Db 1083 TGAGTGTATGGAAGGACGAGACATCATGAGTGCCTGATCTGTGAGCGCCACTAAT 1142
Oy 421 eIleTyrGluGluThrThrAspIleThrPheIleAsnIleHisAspIlePheHisValPhePr 441
Db 1143 TATCTATGAACAAACACAGACATCTGATTAATATCCATGACATCTTCATGTTTTC 1202
Oy 441 oGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPheAr 461
Db 1203 CCAAGTGCACGAAGAGAAATGAGTTATTTTGGCTCTGATTAACAAACAGGTTCCG 1262
Oy 461 gHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysAspSerSerGlyG 481
Db 1263 TCATTTATACAAATATACATCTATTTTAAAGAAAGCAAAATATTAACATCCAGGCGTG 1322
Oy 481 yLeuProLarProSerAspPheLysCysProIleLysGluIleAlaIleThrSerG 501
Db 1323 GCTGCTGCTCCCACT-----GTCAC----- 1344
Oy 501 yGluTrpGluVal-----LeuGly-----ArgH 509
Db 1345 -----TGGATGATCATCATGAGATCTGTAGAACTCATCTGTATGTGTGACACA 1400
Oy 509 sGlySerAsnIleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAs 529
Db 1401 TATAGTTGAGATCCCAAGTTGATGAGTCAAGAGGCTGATATATTTTGAAGCACCAAGA 1460
Oy 529 pSerProLeuGluHisHisLeuTyrValValSerTyrValAsnProGluGluValThrAr 549
Db 1461 CTCCCTTAAAGCATCCAGTACGCTAGTACGATGATTAATCTCGAGAGGTCACAG 1520
Oy 549 gLeuThrAspArgLysTyrSerHisSerCysCysIleSerGlnHisCysAspPhePheI 569
Db 1521 GCTACACTGACCGCTGCTACTCACATTTCTGCTGATCATGACGACTGTGACTTCTTAT 1580
Oy 569 eSerLysTyrSerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerPr 589
Db 1581 AAGTAAGATATGATACCAAGAAATCCACACTGTGTGCTTAAACAAGATACAGTCC 1640
Oy 589 oGluAspAspProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaG 609
Db 1641 TGAAGATGACCACTGTCACAAACAAAGATTTTGGGCCACCATTTTGCATTCAGCAG 1700
Oy 609 yProLeuProAspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheTh 629
Db 1701 TCCTCTCTCTACTACTCTCCAGAAATTTCTTTTGAAGTACTACTGATTTAC 1760
Oy 629 rLeuTyrGlyMetLeuTyrLysProHisAspLeuGlnProGluLysLysTyrProThVa 649
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Db 1761 ATTGTATGGATGCTTCAACAGCCCTCATGATCTACAGCTGGAGAAATATCTACTGT 1820
Oy 649 lLeuPheIleTyrGlyGlyProGluValGlnLeuValAsnAsnArgPheLysGlyVal 669
Db 1821 GCTGTTCTATATGTGTGTCTCTCAGGTGCACTTGTGTATATATCGTTTAAAGAGTCAA 1880
Oy 669 sTyrPheArgLeuAsnThrIleAlaSerLeuGlyTyrValValValIleAspAsnAr 689
Db 1881 GTATTTCCGCTTGAATACCCCTAGCCCTCTAGTGTATGTGTGTGTAGATAGACAAACAG 1940
Oy 689 gGlySerCysHisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnI 709
Db 1941 GGGATCCGTGACCGAGGCGCTTAAATTTGAAGGCGCTTAAATATATAAATG----- 1992
Oy 709 eGluIleAspAspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAs 729
Db 1992 ----- 1992
Oy 729 pLeuAspArgValGlyIleHisGlyTyrPThrSerTyrGlyGlyTyrLeuSerLeuMetAlaLe 749
Db 1992 ----- 1992
Oy 749 uMetGlnArgSerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpI 769
Db 1993 -----GTTGCTATTGCTGGGCGCCAGTCACTCTGTGTGAT 2027
Oy 769 ePheTyrAspThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnI 789
Db 2028 CTCTATATATACAGATACAGAAACGTTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2087
Oy 789 yTyrTyrLeuGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLe 809
Db 2088 CTATTACTTACGATCTGGCGCATGACAGCAAGAAAGTCCCTGATCAACCAATTCGTTT 2147
Oy 809 uLeuLeuLeuHisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLe 829
Db 2148 ACTGCTCTTACATGCTTCCGTGATGAGAAATGTCATTTTGCATATACACTATATTACT 2207
Oy 829 uSerPheLeuValAlaArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgH 849
Db 2208 GAGTTTCTTACTGAGGCGTGAAAGCCATATGATTTA-----CAGGAGAGACA 2255
Oy 849 sSerIleArgValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrLeuG 869
Db 2256 CAGCATAGAGTTCCTGATGCGAGAAACATTATGATGATCTGTTTGCACCTTCA 2315
Oy 869 nGluAsnLeuGlySerArgIleAlaIleAlaLeuLysValIle 882
Db 2316 AGAAACCTTGATCAGCTATTGCTGCTTAAGAAGTGATA 2355

RESULT 13
ABN59775
ID ABN59775 standard; cDNA; 2668 BP.
XX
AC ABN59775:
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 186.
XX
KW Human; antianemic; vulnery; antiinflammatory; immunomodulator;
KW antilefertility; cerebroprotective; cyostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US26015.
XX

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PR 11-SEP-2000: 200005-0659671.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
XX WPI: 2002-292408/33.
DR P-PSDB: ABB97362.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
XX
PS Claim 1: SEQ ID NO 186; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention.
XX
XX
SQ Sequence 2668 BP; 796 A; 564 C; 592 G; 716 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 2668
Score: 3771.00 Matches: 724
Percent Similarity: 82.09% Conservative: 0
Best Local Similarity: 82.09% Mismatches: 0
Query Match: 80.23% Indels: 158
DB: 24 Gaps: 2

US-10-070-464-1 (1-882) x ABBN59775 (1-2668)
QY 1 MetAlaAlaAlaMetGluThrGluGlnLeuGlyValGluIlePheGluThrAlaAspCys 20
DB 234 ATGGCAGCAGCATGCAACAGACACACAGCTGGGTGTAGATATTGTAACCTGGCGACTGT 293
QY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyValGluArgTyr 40
DB 294 GAGGAGATATTGATCAGACGATCGGCTAAATTTGAGGCTTTTATGTGGACGGTAT 353
QY 41 SerTrpSerIleuLysLysLeuLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
DB 354 TCCTGGAGTCAGCTTAAAGCTGCTGGCGATACCGAAATATCATGCTCATCATGATG 413
QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
DB 414 GCTAAGCAGCATGATGATTTTATGTTGTGAAGAGATATCCAGATGAGACCTCATTTCA 473
QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyLysAsnArgLysAsnThrLeuPheTyrSer 100
DB 474 GACAGATCATATTACCTGGCATGTCTGGTGAAGACAGAAATATCACCTGTTTATCT 533
QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTyrLysProLeuLeu 120
DB 534 GAAATTCCTCCAAATCAATCATTAGACGACAGCTTATGCTCTCTTGGAGCCCTTTTG 593
QY 121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
DB 594 GATCTTTTTCAG----- 605
QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
DB 605 ----- 605
QY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180

DB 605 ----- 605
QY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
DB 606 -----CAACAACCTTTTAAGCCCAATCTAGTGAAGAACTAGTGTCTCCACATACAGGATG 659
QY 201 AspProLysLeuCysProAlaAspProAspTyrIleAlaPheIleHisSerAsnAspIle 220
DB 660 GATCCAAATTTATGCCCTGCTGATCCAGACTGAGATTCTTTTATACATACCAACGATATT 719
QY 221 TrpIleSerAsnIleValIThrArgGluGluArgLeuThrTyValHisAsnGluLeu 240
DB 720 TGGATATCTAATCATCTAATACAGAGAAAGAGACTCTATGTGCAATGAGACTA 779
QY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGlu 260
DB 780 GCCACATGGAGAGAGATGCGACATGAGTGGACTGCTTCTTGTCTCCAGAAAGAA 839
QY 261 PheAspArgTyrSerGlyTyrTyrTrpCysProLysAlaGluThrThrProSerGlyGly 280
DB 840 TTTCATAGATATTCTGGCTATTGGTGGTCCCAAAAGCTGAACAACTCCAGTGGTGT 899
QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
DB 900 AAATTCCTTAGAATCTATATGAGAAATGATCAATCTGAGTGGAGAAATTTATTCATGTT 959
QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
DB 960 ACATCCCTATGTTGGAAACAGAGGCGAGATTCATTCCTTAAACAGGTACA 1019
QY 321 AlaAsnProLysValIThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
DB 1020 GCAATCTCTAAAGCTACTTTTAAGATGTCAGAAATATGATGATGCTCGAAGAGATC 1079
QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
DB 1080 ATAGATCTCATAGATTAAGAACTAATTCACCTTTTGAAGATTTGTAAGAGCTTGA 1139
QY 361 TyrIleAlaArgAlaGlyTyrThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
DB 1140 TATATTCACAGAGCTGATGAGTCTGAGGAGAAATATGCTGTGCTCATCTTACTGAT 1199
QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400
DB 1200 CGCTCCAGACTGCCCTACAGATAGTGTGATCTCAGCTGAATATTATTCACAGTAA 1259
QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
DB 1260 GATGATGTTATGGAAGAGAGAGACTCATTCAGTCACTGCTGATTCGTGACGCCACTA 1319
QY 421 IleIleTyrGluGluThrThrAspIleThrIleAsnIleHisAspIlePheHisValPhe 440
DB 1320 ATTATCTATGAAGAAACAGACATCTGATTAATTCATGACATCTTTCATGTTT 1379
QY 441 ProGlnSerHisGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
DB 1380 CCCCAAGTCAAGAGAGAAATTTGATTTATTTTCCCTGATGATCCAAACAGGTTTC 1439
QY 461 ArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
DB 1440 CGTCATTTATACAAATTTACATCTATTTTAAAGCAAGCAAAATTTAAACATCCAGTGT 1499
QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
DB 1500 GGGCTGCTGCTCCCAAGTGAATTCAGTGTCTATCAAGAGGAGATGAGAAATTTACAGT 1559
QY 501 GlyIleuTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
DB 1560 GGTGAATGGGAGATCTTGGCCGCGCATGATCTAATTCACAGTTCGTAAGTCAGACAG 1619
QY 521 LeuValTyrPheGluGluGlyThrLysAspSerProLeuGluHisHisLeuTyrValValSer 540
DB 1620 CTGCTATATTTTGAAGGACACCAAGACTCCCTTTAGAGCATCACCTGATGATGAGT 1679

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QY 541 TyValaAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
    |||||
Db 1680 TACCTAAATCCTGGAGAGGAGGACAGGCTGACCGCTGCTACTCTTCTGCTGC 1739
QY 561 HisSerGlnHisCysAspPhePheHisSerLysTyrSerAsnGlnLysAsnProHisCys 580
    |||||
Db 1740 ATCAGTCAGCAGCTGACTCTTATATAGTAAAGTAAACAGAAATCCACACTGT 1799
QY 581 ValSerLeuTyrLysLeuSerSerProGlnAspAspProThrCysLysThrLysGluPhe 600
    |||||
Db 1800 GTGCTCCCTTACAGCATATACGCTGAAGATGACCACTTGCACAAAGAAATTT 1859
QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
    |||||
Db 1860 TGGGCCACCACTTTGGATTCAGCAGGCTCTTCTCTGACTATCTCTCCAGAAATTTTC 1919
QY 621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
    |||||
Db 1920 TCTTTTGAAGTACTACTGATTCGATTTACATTTGATGATGCTCTACAAAGCCATGATCTA 1979
QY 641 GluProGlyLysLysTyrProThrValLeuPheIleTyrGlyGlyProGlnValGlnLeu 660
    |||||
Db 1980 CAGCTCGAAGAAATATCCCTACTGCTCTGTTCAATATGGTGGTCTCTCAG----- 2030
QY 661 ValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsnThrLeuAlaSerLeuGly 680
    |||||
Db 2030 ----- 2030
QY 681 TyrValValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluGly 700
    |||||
Db 2030 ----- 2030
QY 701 AlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnTyr 720
    |||||
Db 2030 ----- 2030
QY 721 LeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTyrPserTyr 740
    |||||
Db 2030 ----- 2030
QY 741 GlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaIle 760
    |||||
Db 2031 ----- 2031
QY 761 AlaGlyAlaProValThrLeuTyrPheTyrAspThrGlyTyrThrGluArgTyrMet 780
    |||||
Db 2040 GCTGGGGCCAGCTACTCTGTGATCTCTATGATACAGATACACGAAACGTTATATG 2099
QY 781 GlyHisProAspGlnAsnGlnGlyTyrTyrLeuGlySerValAlaMetGlnAlaGlu 800
    |||||
Db 2100 GGTCCACCTGACCAAGATGAACAGGCTATTAAGTATGTCGGCATCCAGCAGAA 2159
QY 801 LysPheProSerGluProAsnArgLeuLeuLeuLeuHisGlyPheLeuAspGlnAsnVal 820
    |||||
Db 2160 AAGTCTCCCTCTGAACCAATCGTTTACTGCTTACATGGTTCCCTGGATGACAAATGTC 2219
QY 821 HisPheAlaHisThrSerIleLeuLeuSerPheLeuValArgAlaGlyLysProTyrAsp 840
    |||||
Db 2220 CATTTTCACATACCATATATATCTAGTTTTCAGAGGCTGGAACCATATGAT 2279
QY 841 LeuGlnIleTyrProGlnGluArgHisSerIleArgValProGluSerGlyGluHisTyr 860
    |||||
Db 2280 TTACAGATCATCTCTCAGAGAGACACAGCATAGAGTCTCTGAATCGGAGACATTAAT 2339
QY 861 GluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySerArgIleAlaIleLeuLys 880
    |||||
Db 2340 GAATCTGATCTTTTGGCTACCTTCAAGAAACCTTGATTCACGATTTGCTGCTAATA 2399
QY 881 ValIle 882
    |||||
Db 2400 GTGATA 2405

```

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RESULT 14
ABK83328
ID ABK83328 standard; cDNA; 4309 BP.
XX
AC ABK83328;
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPRP-1 splice variant #4.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyskinesia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US31874.
XX
PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR ) FERRING BV.
XX
PI Q1 S, AKinsanya KO, Riviere PJ, Junten J;
XX
DR WPI; 2002-444178/47.
XX
DR P-PSDB; ABG61597.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
XX
XX
PS Disclosure: Page 67-68; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypertension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4309 BP; 1304 A; 790 C; 907 G; 1308 T; 0 other;
XX
Alignment Scores:
Pred. No.: 0 Length: 4309
Score: 3661.50 Matches: 708
Percent Similarity: 80.09% Conservative: 0
Best Local Similarity: 80.09% Mismatches: 1
Query Match: 77.90% Indels: 176
DB: 24 Gaps: 1
US-10-070-464-1 (1-882) x ABK83328 (1-4309)
QY 1 MetaAlaAlaMetGluThrGlnGluGlyValGluIlePheGluThrAlaAspCys 20
    |||||
Db 214 ATGGCAGCAGCATGTAAGACAGACAGCTGGGTGTGAGATATTGAACTCGGACTGT 273

```


QY 21 GluGluAsnIleGluSerGlnAspArgProLysLeuGluProPheTyrValGluArgTyr 40
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 Db 274 GAGGAGATATTTGAATCACAGATCGCCTAATGAGACCTTTTATATGTTGAGCGGTAT 333
 QY 41 SerTrpSerGlnLeuLysLysLeuAlaAspThrArgLysTyrHisGlyTyrMetMet 60
 |||||
 Db 334 TCTGGAGTCAGCTTAAAGCTGCTGGCCGATACAGAAATATCATGTGCTCATGATG 333
 QY 61 AlaLysAlaProHisAspPheMetPheValLysArgAsnAspProAspGlyProHisSer 80
 |||||
 Db 394 GCTAAGGACACCATGATTTTCATGTTGTCAAGAGATATATCTCGAAGAGACTATTAAGA 453
 QY 81 AspArgIleTyrTyrLeuAlaMetSerGlyLysAsnArgLysAsnThrLeuPheTyrSer 100
 |||||
 Db 454 GACAGATCATATACCTGCTGCTGCGAGACAGACAAATACACTGTTTATCT 513
 QY 101 GluIleProLysThrIleAsnArgAlaAlaValLeuMetLeuSerTrpLysProLeuLeu 120
 |||||
 Db 514 GAAATTCCTCAAACTATCATATAGAGACAGCTTAACTGCTCTTGGAAAGCCTCTTTTG 573
 QY 121 AspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuArg 140
 |||||
 Db 574 GATCTTTTCAGGCAACACTGACGACTATGCAATGATATCTCGAAGAGAGACTATTAAGA 633
 QY 141 GluArgLysArgIleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGly 160
 |||||
 Db 634 GAAAGAAACGCAATGAGACAGTCGGAATGCTTACATATTATCCACAGGAAGTGA 693
 QY 161 ThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGly 180
 |||||
 Db 694 ACATTTCTGTTTCAAGCCGCTAGTGGAATTTATCAGCTAAAGATGAGGCGCACAGGA 753
 QY 181 PheThrGlnGlnProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMet 200
 |||||
 Db 754 TTATCCGCAACACCTTTAAGGCCCATCTAGTGGAAACTGTTGTTCCCAACATACGGATG 813
 QY 201 AspProLysLeuCysProAlaAspProAspTrpIleAlaPheIleHisSerAsnAspIle 220
 |||||
 Db 814 GATCCAAATTTATGCTGCTGCTGATCCAGACTCGATTGCTTTATACATACCAAGATATT 873
 QY 221 TrpIleSerAsnIleValThrArgGluArgGluArgLeuThrTyrValHisAsnGluLeu 240
 |||||
 Db 874 TGGATATCTTACATCGTAAACCCAGAGAAAGAGAGACTCATATGCGCAATGAGCTA 933
 QY 241 AlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGlu 260
 |||||
 Db 934 GCCAATCATGAAAGATGCGACATCAGCTGAGTCCGCTACTTGTGTTCCCAAGAAAGAA 993
 QY 261 PheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGluThrThrProSerGlyGly 280
 |||||
 Db 994 TTTGATAGATATTTCTGCTATTTGCTGCTGCCAAAGCTGAACAACTCCACGTGGTGT 1053
 QY 281 LysIleLeuArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisVal 300
 |||||
 Db 1054 AAATCTTATGATTTCTATATGAAAGAAATGAGAAATCTGAGGTGGAATATTCATGTT 1113
 QY 301 ThrSerProMetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThr 320
 |||||
 Db 1114 ACATCCCATATGTTGGAACAAAGAGAGCGCATTCATCCGTTATCTCTAAACAGGTACA 1173
 QY 321 AlaAsnProLysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIle 340
 |||||
 Db 1174 GCAAATCCCTAAAGTCACTTTTAAAGATGTCAGAAATATGATGCTGTAAGGAAGATC- 1232
 QY 341 IleAspValIleAspLysGluLeuIleGlnProPheGluIleLeuPheGluGlyValGlu 360
 |||||
 Db 1232 ----- 1232
 QY 361 TyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyrAlaTrpSerIleLeuLeuAsp 380
 |||||
 Db 1232 ----- 1232
 QY 381 ArgSerGlnThrArgLeuGlnIleValLeuIleSerProGluLeuPheIleProValGlu 400

Db 1232 ----- 1232
 QY 401 AspAspValMetGluArgGlnArgLeuIleGluSerValProAspSerValThrProLeu 420
 |||||
 Db 1232 ----- 1232
 QY 421 IleIleTyrGluGluThrThrAspIleTrpIleAsnIleHisAspIlePheHisValPhe 440
 |||||
 Db 1232 ----- 1232
 QY 441 ProGlnSerHisGluGluGluIleGluPheIlePheAlaSerGluCysLysThrGlyPhe 460
 |||||
 Db 1232 ----- 1232
 QY 461 ArgHisLeuTyrIleThrSerIleLeuLysGluSerLysTyrLysArgSerSerGly 480
 |||||
 Db 1232 ----- 1232
 QY 481 GlyLeuProAlaProSerAspPheLysCysProIleLysGluGluIleAlaIleThrSer 500
 |||||
 Db 1232 ----- 1232
 QY 501 GlyGluTrpGluValLeuGlyArgHisGlySerAsnIleGlnValAspGluValArgArg 520
 |||||
 Db 1233 -----CAAGTGATGAAGTCAGAGC 1253
 QY 521 LeuValTyrPheGluGlyTyrThrLysAspSerProLeuGluHisIleuTyrValValSer 540
 |||||
 Db 1254 CTGCTATATTTTAAAGGACACCAAGACTCCCTTTAAGCATCACCGTACGATGACGT 1313
 QY 541 TyrValAsnProGlyGluValThrArgLeuThrAspArgGlyTyrSerHisSerCysCys 560
 |||||
 Db 1314 TACGTAATCTCGAAGAGTGACAGAGCTACGACCGTGCCTACTACTTCTTCTGCTGC 1373
 QY 561 IleSerGlnHisCysAspPhePheIleSerLysTyrSerAsnGluLysAsnProHisCys 580
 |||||
 Db 1374 ATCAGTCAGCACTGTGACTTCTTATAGTAAGTATAGTAACCAAGAAATCCACACTGT 1433
 QY 581 ValSerLeuTyrLysLeuSerSerProGluAspAspProThrCysLysThrLysGluPhe 600
 |||||
 Db 1434 GTGTCCTTTTACAAAGCTATCAAGTCTGAGAGATGACCACCTGCAAAACAAAGGAATTT 1493
 QY 601 TrpAlaThrIleLeuAspSerAlaGlyProLeuProAspTyrThrProProGluIlePhe 620
 |||||
 Db 1494 TGGGCCACCTTTTGGATTTCAGCAGGTCCTCTCTGACTATATCTCTCCAGAAATTTTC 1553
 QY 621 SerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeuTyrLysProHisAspLeu 640
 |||||
 Db 1554 TCTTTGAAAGTACTACTGATTTACATTGTATGGGATGCTTACAAAGCCTCATGATCTA 1613
 QY 641 GlnProGlyLysLysTyrProThrValLeuPheIleTyrGlyGly--ProGlnValGlnL 660
 |||||
 Db 1614 CACCTCGAAGAAAGAAATATCTTACTGTGCTGTCATATATGCTGTCCTCCAGGTGAGT 1673
 QY 660 euValAsnAsnArgPheLysGlyValLysTyrPheArgGluAsnThrLeuAlaSerLeuG 680
 |||||
 Db 1674 TGGTGATATATCGGTTTAAAGAGAGTCAAGTATTTCCGCTTGAATACCCTTCTCTAG 1733
 QY 680 LysThrValValValIleAspAsnArgGlySerCysHisArgGlyLeuLysPheGluG 700
 |||||
 Db 1734 GTTATGTGGTGTGATGATGATGACACAGGAGATCTGTCAACGAGGCTTAATTTGAAG 1793
 QY 700 LysAlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGlnValGluGlyLeuGlnT 720
 |||||
 Db 1794 GCGCCTTTAAATATAAATGCGTCAATATGAAATTAACGATGCGTGAAGGACTCCAAAT 1853
 QY 720 TyrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGlyIleHisGlyTrpSerT 740
 |||||
 Db 1854 ATCTACGCTTTCATATGATTTTACATTGACTTACATGCTGTGGGCAATCCAGCGTGTCTCT 1913
 QY 740 TyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAspIlePheArgValAlaI 760
 |||||

cc comprises: (a) an oligo-*at* primer and an oligonucleotide complementary

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395 LeupheIlleProValGluspaSpvalMetGlunArgGlunArgLeuIlleglUserValPro 414
qy

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|||||
Db 601 TTTTATCCAGTAGAGATGATGTTATGGAAGCAGACTCATTCAGTAGTCCT 660
QY 415 AspSerValThrProLeuIleIleTyrGluGluThrThrsplleThrleuIleHis 434
Db 661 GATTCTGTGCGCCACTAATATATATGAAAGAAACAACACATCTGGATTAATATCCAT 720
QY 435 AspIlePheHisValPheProGlnSerHisGluGluIleGluPheIlePheIleSer 454
Db 721 GACATCTTTCATGTTTTCCTCCCAAGTCAAGAGAGAAATTCAGTTTATTTTGGCTCT 780
QY 455 GluCysLeuThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGluSerLys 474
Db 781 GAATGCAAAACAGGTTCCTCATTTATCAAAATTAACATCTATTATTAAGCAAGCAAA 840
QY 475 TyrLeuArgSerSerGlyLeuProAlaProSerAspPheLysCysProIleLysGlu 494
Db 841 TATTAACGATCCAGTGTGGTGGCTGCTCCCAAGTGATTTCAAGTGTCTTATCAAGAG 900
QY 495 GluIleAlaIleThrSerGlyLeuTyrPgluValIleuGluYargHisGluSerAnIleGln 514
Db 901 GAGATAGCATATTCAGTGGTGAATGGAAAGTCTTGCGCGCATGGATCTATATCCAA 960
QY 515 ValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeuGluHis 534
Db 961 GTTGATGAAGTCAAGAGGCTGTATATTTTGAAGCACCACAAAGACTCCCTTATGAGCAT 1020
QY 535 HisLeuTyrValValSerTyrValAsnProGluValThrArgLeuThrAspArgGly 554
Db 1021 CACCTTACCTACTGACTGATTACGTAATCTCGAGAGGTGACAAGCTGAGTACCGTAGC 1080
QY 555 TyrSerHisSerCysLysIleSerGlnHisCysAspPhePheIleSerLysTyrSerAsn 574
Db 1081 TACTACATCTCTGTCGATCAGTCACTGACACTGTGACTTCTTATTAAGTAGTAGTAAGAC 1140
QY 575 GlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAspAspProThr 594
Db 1141 CAGAAACATCCACACGTGTGTCTTTCACAACTATCAAGTCTGAGATGACCCAACT 1200
QY 595 CysLeuThrLysGluPheThrAlaThrIleLeuAspSerIleGluProLeuProAspTyr 614
Db 1201 TGCAGAACAAAGAAATTTTGGCCACCATTTTGGATTCCACAGATCTCTCTCGACTAT 1260
QY 615 ThrProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGlyMetLeu 634
Db 1261 ACTCCTCCAGAAATTTTCTCTTTTGAAGTACTACTGATTTACATTTGATGGATGCTC 1320
QY 635 TyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIleTyrGly 654
Db 1321 TACAAACCTCATGATCTACAGCTCGAAGAAATATCTACTGCTGTTCAATATATGCT 1380
QY 655 GlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArgLeuAsn 674
Db 1381 GGTCTCCAGTGCAGTGTGTAATTCGTTTAAAGAGTCAAGTATTTCCCGCTTGAAT 1440
QY 675 ThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgLysSerCysHisArg 694
Db 1441 ACCCTAGCCTCTCTAGTATGTTGTTGATGATAGACAAACAGGGGATCTCTCACCGA 1500
QY 695 GlyLeuLysPheGluGluValAlaPheLysTyrLysMetGlyGlnIleGluIleAspAspGln 714
Db 1501 GGCTTTAAATTTGAAAGCCCTTTAAATATAAATG----- 1536
QY 715 ValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArgValGly 734
Db 1536 ----- 1536
QY 735 IleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArgSerAsp 754
Db 1536 ----- 1536
QY 755 IlePheArgValAlaIleAlaGlyAlaProValThrLeuTyrPhePheTyrAspThrGly 774
|||||

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Db 1537 -----GTTCCTATTGCTGGGCCCCAGTCACTCTGTGATCTTCTATGATACAGCA 1587
QY 775 TyrThrGluArgTyrMetGluHisProAspGlnAsnGluGlnGlyTyrTyrLeuGlySer 794
Db 1588 TACACGGACGTTATATATGGTTCACCTGACCAAGAAATGAACAGGGCTATTAATCTTAGATCT 1647
QY 795 ValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuHisGly 814
Db 1648 GTGCGCATGACACAGAAAGATTCCCTCGAACCAATATGTTTACGCTTACATAGCT 1707
QY 815 PheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeuValArg 834
Db 1708 TTCTGGATGAGATGTCATTTTGGACATACACAGTATATTAAGTATCTTTTATGAGAGC 1767
QY 835 AlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArgValPro 854
Db 1768 GGTGGAAGCCATATGATTTTACAGATCTTATCCAGGAGACACACATTAAGAGTTCCT 1827
QY 855 GluSerGlyLysHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeuGlySer 874
Db 1828 GAATCGGAGACATTTATGAACATGATCTTTGACACTTCAACAGAAACCTTGATCA 1887
QY 875 ArgIleAlaIleLeuLysValIle 882
Db 1888 CGTATGTCTCTCTAAAGTGATA 1911

RESULT 16
ABK83323
ID ABK83323 standard; CDNA; 2617 BP.
XX
AC ABK83323:
XX
DT 12-AUG-2002 (first entry)
XX
DE cDNA encoding human DPPIV related serine protease DPP-2.
XX
KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPPP;
KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW dyslexia; reproductive disorder; inflammatory disorder;
KW metabolic disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200231134-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001: 2001MO-US31874.
XX
PR 12-OCT-2000: 2000US-240117P.
XX
PA (FERR ) FERRING BV.
XX
PI Qi S, Akinsanya KO, Riviere PJ, Junten J;
XX
DR WPI; 2002-444178/47.
XX
PT P-PSDB; ABG61592.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
XX
PS Claim 1; Page 56-57; 113pp; English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly

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CC infectiots caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychiatric and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABRK33322-ABRK3343 encode human DPR proteins.

SQ Sequence 2617 BP; 558 A; 830 C; 736 G; 493 T; 0 other;

Alignment Scores:	
Pred. No.:	4,04e-283
Score:	2870.00
Percent Similarity:	77.958
Best Local Similarity:	61.558
Query Match:	61.06%
DB:	24
	Gaps: 2
	Indels: 2
	Matches: 517
	Conservative: 134
	Mismatches: 187
	Length: 2617

US-10-070-464-1 (1-882) x ABK83323 (1-2617)

QY	35	PheYrValGluArgTyrSerTrpSerGlnLeuLysLysLeuAlaAspTrnArgLys	54
Db	80	TTTCAGGTGAGAAAGCACTGGTGGAGCGGCTCCGGAGCATTCACCGGACCCCAAG	139
QY	55	TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsp	74
Db	140	TACTCGGGCCCATGTTCACACAGGGCCCCACAGACTTCCAGTTTGTGGCAGAAAGCAGAT	199
QY	75	ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyLysAsnArgGlu	94
Db	200	GAGCTGGGGCCCCACTCCACCGGCTCTACTACTGGGATGCGATATGCGACCCGAGAC	259
QY	95	AsnThrIlePheTyrSerGluIleProLysThrIleAsnArgAlaAlaValMetLeu	114
Db	260	AACCTCCCTCTACTCTGTGAGATTCACCAAGAAAGTCCGGAAGAAGGCTGTGGCTCTCTG	319
QY	115	SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg	134
Db	320	TCTGTGAAGCAGAGATGCTGGATCATTTCCAGGCCACGCCCAACCATGGGGCTACTCTCGG	379
QY	135	GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp	154
Db	380	GAGAGAGGCTGCTGAGAGGAGCGGAAACGCCCTGGGGGCTTTCGGCATCACCTCTACGAC	439
QY	155	TyrHisGlnGlySerGlyTyrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys	174
Db	440	TTTCCACACGAGAGATGGCTTCCTTCTTCCAGGCCACGACACACCTCTTCCACTGTGCG	499
QY	175	AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluTrnSer	194
Db	500	GACGGCGGCAAGAACGGCTTCATGCTGTCTCCCTATGAACCGCGTGAACATCAGACCCAG	559
QY	195	CysProAsnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe	214
Db	560	TGCTCAGAGGCCCCGGAAGGAGACCCCAAAATGTGCTCCGACACCTGCTCTTCTCTCTC	619
QY	215	IleHisSerAsnAspIleTyrPheSerAsnIleValThrArgGluGluArgGlyLeuThr	234
Db	620	ATCATATACACGCACTGTGGGTGGCCCAACATCGACAGACAGGAGCGCGCGGTGACC	679
QY	235	TyrValHisAsnGluLeuAlaAsnMetGlnAlaAspAlaArgSerAlaGlyValAlaTrn	254
Db	680	TTTCGCCACCAAGTTATTCACATGTCCTGGATGACCCCAAGTCGTGGGTGTGGCCACC	739
QY	255	PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTrpCysProLysAlaGlu	274
Db	740	TTTCTCATACAGAGAGATTCGACCCGCTCATGTGGATAGTGTGTGCCACACGCTCC	799
QY	275	ThrTrnProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspGluSer	293
Db	800	TGGGAAAGTTTCAGAGGGCTTCAGAACACCTTCGAAATCCTGTATAGAGAAAGTCATGTAGTCC	859

OY	294	GLIValGluIleIleHISValThrSerProMetLeuGluThrArgArgLysAspSerPhe	313
Db	860	GAGGGGAGGTCATTCAAGTCCTCCCTCCCGCTGAAAGAAAGACGGAGCTGAT	919
OY	314	ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerLuuLleMet	333
Db	920	CGGTACCCACAGACAGGACACAGAAATCCCAATGGCTTGAACCTGGCTAGTTCCAG	979
OY	334	ILEAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu	353
Db	980	ACTGACAGCCGAGGCAAGATCGTCGACCACGAGAGAGAGAGCTGGTCGACCCCTTTCAGC	1038
OY	354	ILEuPheGluGlyValIGlyTyrIleAlaArgAlaGlyThrPheProGluGlyLysTyr	373
Db	1040	TTCGCTGTTCCCGAAGGGAGATACATGCCAGGCGCGGTTGAGCCCGGATGGCAATATC	1098
OY	374	AlATrpSerIleLeuLeuAsnArgSerGlnThrArgLeuGlnIleValLeuLeuSerPro	393
Db	1100	GCGTGGCGCATGTCCTCGAGACGGGCCACAGATGGCTCGAGTGTCTCTCCGCCCGG	1158
OY	394	GLIuPheIleProValIGluAspAspValMetGluArgGlnArgLeuIleGluSerVal	413
Db	1160	GCCCTGTTCATCCGACACAGAGAAATGAGAGACAGCGGTAGCTTCGACAGCTGTC	1218
OY	414	ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle	433
Db	1220	CCCGAGATGTGCACCGGCTATGTGGTATGAGAGAGTCAACACCTCTGGATCAATGTT	1278
OY	434	HISAspIlePheHISValPheProGlnSerHIS---GluGluGluIleGluPheIlePhe	452
Db	1280	CATGCATCTCTATCCCTTCCCCCAATCAGAGGAGAGAGACGCTGTCTTCGCCG	1338
OY	453	AlAserGluCysLysThrGlyPheAlaGlnHISLeuTyrLysIleIleHISerIleLeuLysGlu	472
Db	1340	GCCATGATATGCAGACCGGCTTCTGCCATTGTACAAATCATCCGCCCTTTTAAATCC	1398
OY	473	SerLysTyrLysAspSerSerGlyLysLeuProAlaProSerAspPheLysCysProIle	492
Db	1400	CAGGCTACGATTTGGATGAGACCCCTTACGCCCGGGGAAGATGAATTTAAGTCCCAT	1458
OY	493	LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGluArgHISGlySerAsn	512
Db	1460	AAGGAGAGATTTGCTGTCGACACGCGGATGAGAGATTTGGCGACGACCGCTTCAAG	1518
OY	513	IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu	532
Db	1520	ATCTGGGTCATGTGGAGACCAAGCTGTGTACTTCCAGGGCACCAAGACAGCCGGCTG	1578
OY	533	GluHISHisLeuTyrValAlaSerTyrValAsnProGlyGluValThrArgLeuThrAsp	552
Db	1580	GAGCACCACTCTACGTGGTACAGTATGAGCGGGCGGAGATCTATAGCTTCAACAG	1638
OY	553	ArgGlyTyrSerHISSerCysLysIleSerGlnHISCysAspPheIleSerLysTyr	572
Db	1640	CCCGGCTTCTCCCTACTCTCTCATGAGCCCAAACTTGACATGTGTTCCGACCAATAC	1698
OY	573	SerAsnGluAsnProHISCysValSerLeuTyrLysLeuSerSerProGluAspAsp	592
Db	1700	AGCAGCCGTGAGACCGCGCCCTGGTGTACAGTTCACAGCTGAGCGGCCGACAGAGAC	1758
OY	593	ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	1760	CCCCGTCACAAAGACGCCCGCTTCTGGGCTAGCATGATGAGAGCAACCGAGTCCGCCCGG	1818
OY	613	AspTyrThrProProGluIlePheSerPheGluSerThrGlyPheThrLeuTyrGly	632
Db	1820	GATTATCTTCTCCAGAGATCTTCATTTCCACACCGCTCCGAGTGGCGCTTACAGCG	1878
OY	633	MetLeuTyrLysProHISAspLeuGlnProGlyLysLysTyrProThrAlaLeuPheIle	652
Db	1880	ATGATCTTACAAAGCCCAAGCTTTCAGGCCACGAGGAAAGAACACCCCAACGCTCTTTTGA	1938

Oy	653	TYTIGLYLPROGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg	672
Db	1940	TATGAGAGCCCCAGGTGACGACTGGTGAATTAACCTCTTAAGAGGATCAAGACTTCGG	1999
Oy	673	LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgGlySerCys	692
Db	2000	CTCAACACACTGGCGTCCCGGGCTACGGCGGTGTGTATGTAGACGAGGGGCTCCT	2059
Oy	693	HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGlnIleAsp	712
Db	2060	CAGCGAGGGCTTGCTTCGAAAGGGGCCCTGAAAAAACCAATGGCCAGGTGAGATCGAG	2119
Oy	713	AspIleValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732
Db	2120	GACCAAGGTGAGGGCCCTGCAGTTCGtGGCCGGAAGAAATGAGCTTATGACCTTGCCGA	2179
Oy	733	ValGlyIleHisGlyTyrPseTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2180	GTTGCCATTCATGGCTGGTCTCTAGGGGGGCTTCCTGCTCATGGGCTAATCCACAG	2239
Oy	753	SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp	772
Db	2240	CCCCAGGTGTTCAAAGGGGCCATCGCGGGTGCCCGCGTCACTGGATGGCTACAGAC	2299
Oy	773	ThrIleTyrThrGlnArgTyrMetGlyHisProAspGlnAsnGluGlnGlyTyrTyrIleu	792
Db	2300	ACAGAGGTACCTAGCGGCTACATGAGACGTCTGAAACAAACACACACGGCTATGAGCG	2359
Oy	793	GlySerValAlaMetGlnAlaGlyLysPheProSerGlyProAsnArgLeuLeuLeu	812
Db	2360	GTTTCGCTGGCCCTGCACGCTGGAGAACCTGCCAATGAGACCCACCGCTTGCTTATCCTC	2419
Oy	813	HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu	832
Db	2420	CACGCGTCTCTGAGCAAGAAACGTGCACATTTCCTACACAACTCTCGTCCCACTG	2479
Oy	833	ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerTlearg	852
Db	2480	ATCCGACAGGGAACCTTACGAGCTCCAGATCTACCCCAAGGAAGACAGTATTGCC	2539
Oy	853	ValProLysSerGlyGlnHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGlnLysLeu	872
Db	2540	TGCCCCAGTCGGGCGAGCACTGTGAAGTCAGCTTGCTCCTCTTCTACAGGAATACCTC	2599
RESULT 17			
ID	ABK83335	standard: cDNA: 4219 BP.	
AC	ABK83335:		
XX	12-AUG-2002	(first entry)	
DE	cDNA encoding human DPRP-2 splice variant #3.		
XX	Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;		
KM	DPRP; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;		
KW	diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;		
KW	heart failure; hypertension; urinary retention; osteoporosis; cancer;		
KW	ulcer; allergy; cancer; psychotic disorder; neurological disorder;		
KM	dyskinesia; reproductive disorder; inflammatory disorder;		
XX	metabolic disorder; gene: ss.		
XX	Homo sapiens.		
OS	MO2002J1134-A2.		
PN	18-APR-2002		
PD	12-OCT-2001.	2001MO-US31874.	
PF	12-OCT-2000.	2000US-240117P.	
XX	12-OCT-2000.	2000US-240117P.	
XX	(FERR) FERRING BV.		

xx Qi S, Akinsanya KO, Riviere PJ, Junien J:
PI WPI; 2002-444178/47.
xx P-PSDB; ABG61604.
DR
xx New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
xx -
PS Disclosure; Page 84-85; 113pp; English.
xx

CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyslexias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABR63322-ABR63343 encode human DPRP proteins.

XX Sequence 4219 BP; 908 A; 1320 C; 1190 G; 801 T; 0 other;

Alignment Scores:

Pred. No.:	8.4e-383	Length:	4219
Score:	2870.00	Matches:	517
Percent Similarity:	77.50%	Conservative:	134
Best Local Similarity:	61.55%	Mismatches:	187
Query Match:	61.06%	Indels:	2
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x ABK83335 (1-4219)

[illegible]

Db	916	TTGCTCAGGGCCCCGGATGGACCCCAAAATGTGCCCTGCCGACCCCTGCTTCTTCCTTC	975
Qy	215	ILeHisSerAsnAspIleThrPileSerAsnIleValThrArgGluGluNArgArgLeuThr	234
Db	976	ATCATATACACGCGACCTGGTGTCGCAACATCGACAGCAGCGAGAGCGCGCTGCAC	1035
Qy	235	TYrValHisAsnGluLeuAlaAsnMetGluGluAspAlaIleArgSerAlaGlyValAlaThr	254
Db	1036	TTTCGCCACCAAGGTTTTATCCATATGTCGTGGATGCCCAAGCTGTGGGTGTGGCCAC	1095
Qy	255	PhenValLeuGluGluGluPheAspArgTYrSerGlyTYrTTPCybProLysAlaGlu	274
Db	1096	TTCCGTCATACAGGAAGATTCGCACCGCTTCATCGGTACTGGGNGGCCACACCTCC	1155
Qy	275	ThrThrProSerGlyGly---LysIleLeuArgIleLeuTYrGluGluAsnAspLeuSer	293
Db	1156	TGGGAAGGTTGAGGGCCCTCAAGACGCTGCATCTGTATAGAGAAATCATATAGTCC	1215
Qy	294	GluValGluIleIleHisValThrSerProMetLeuGluThrArgAlaLysSerPhe	313
Db	1216	GAGGTGAGAGTCATTCACGTCCCTCCCTCCGCTTGAGAAAGAACAGCAGCTCAT	1275
Qy	314	ArgTYrProLysThrGlyThrAlaAsnProLysValThrPhenLysMetSerGluLeuLeu	333
Db	1276	CGGTACCCACAGACAGGACACAGAAATCCCAAGATTGCTTGAACCTGGCTGAGTTCCAG	1335
Qy	334	IleAspAlaGluGluArgIleIleAspValIleAspLysGluLeuIleGluProPheGlu	353
Db	1336	ACTGACACCCAGGGCAGATGTCTGCACCCAGAAAGAGAGACTGTGTGAGCCCTTCAGC	1395
Qy	354	IleLeuPheGluGluValGluTYrIleAlaArgAlaGlyTYrThrProGluGlyLysTYr	373
Db	1396	TGCGCTGTCCGAGAGGTGGAGTACATCGCCAGCGCGGTGACCCGGATGCAAAATAC	1455
Qy	374	AlaThrSerIleLeuLeuAspArgSerGluThrArgLeuGluIleValLeuLeuSerPro	393
Db	1456	GCTTGCGGCATGTTCTCGTGCACCGGCCACAGCTGCTTCAGCTGTCTCTCTCCCTCCG	1515
Qy	394	GluLeuPheIleProValGluAspAspValMetGluArgGluIleGluSerVal	413
Db	1516	GCCCTGTCATCCCGACACAGAAATGAAGACGCGCTGAGCTTCGACAGACTGTC	1575
Qy	414	ProAspSerValThrProLeuIleIleTYrGluGluThrThrAspIleThrPheAsnIle	433
Db	1576	CCGAGGAATGTCCAGCCGTATGTGGTACAGAGAGTCCACACAGCTGTGATCATGTT	1635
Qy	434	HisAspIlePheHisValPheProGluSerHis---GluGluGluIleGluPheIlePhe	452
Db	1636	CATGACATCTGTATCCCTTCCCCCAATGACAGAGAGAGAGAGACTGTGCTTCTCTCCG	1695
Qy	453	AlaSerGluCysLysThrGlyPheArgHisLeuTYrLysIleThrSerIleLeuLysGlu	472
Db	1696	GCCATATGATCAAGACCGGCTTCTGCCAATTTGTACAAAGTCCACCGCTTTTAAATCC	1755
Qy	473	SerLysTYrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle	492
Db	1756	CAGGCTACATTTGGATGTGACCCCTTCAGCCCGGGGAAGATGAATTTAAGTCCCTTT	1815
Qy	493	LysGluGluIleAlaIleThrSerGlyGluTYrPglValValLeuGlyArgHisGlySerAsn	512
Db	1816	AAGCAAGAGATTTGCTCTGACCACCGGATATGGAGAGTTTGGCAGAGCAGCTCCAAAG	1875
Qy	513	IleGluIleAspGluValArgArgLeuValTYrPheGluGlyThrLysAspSerProLeu	532
Db	1876	ATCTGGGGTCATATGAGACCAACAGCTGGTGTACTTCCAGAGCACAAGGACAGCGCGTG	1935
Qy	533	GluHisHisLeuTYrValValSerTYrValAsnProGlyGlyValThrArgLeuThrAsp	552
Db	1936	GAGACACACCTCTACGTTGTCAGTATGAGAGCCGCCGCGGACATCTGACCTCACACG	1995
Qy	553	ArgGlyTYrSerHisSerCysLysIleSerGlnHisCysAspPheIleSerLysTYr	572

Dd	1996	CCGGCTTCTCCCACTACCTGCTCCATGAGCAGCAAGAACTTGACATGTTGTCAGGCACATAC	205
Qy	573	SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluAsp	592
Dd	2056	AGCAGCGAGACACAGCGCCCTCGTGCACGCTTCAACACTGACGCCCGCAGCACAC	2115
Qy	593	ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Dd	2116	CCCCGCACAAAGCAGCCCGCTTCTGGCTAGCATGATGAGGACAGCCAGCTGCCCGC	2175
Qy	613	AspTyrThrProGluIlePheSerPheGluSerThrGlyPheThrLeuTyrGly	632
Dd	2176	GATTATGTCCTCCAGAGATCTTCATTTCACACGCGCTCGAGATGTCGGCTACAGC	2235
Qy	633	MetLeuTyrLysProHisAspLeuGlnProGluLysLysTyrProThrValLeuPheIle	652
Dd	2236	ATGATCTCAAGGCCCAAGCGCTTCGACGCCAGGAAACACCCCAACGCTCTTGTGA	2295
Qy	653	TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg	672
Dd	2236	TATGAGAGCCCCAGAGTGCAGCTGGAGATTAACCTCTTAAAGGATCACTACTGGG	2355
Qy	673	LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgGlySerCys	692
Dd	2356	CTCAACACACGCGCTCCCGGGCTACGCGGTGGTGTGATTAAGCGAGGGGCTCTGT	2415
Qy	693	HisArgGlyLeuLysPheGluGlnAlaPheLysTyrLysMetGlnIleGlnIleAsp	712
Dd	2416	CAGCAGGCGCTCCGCTTCGAAGGGCCCTGAATAAACCAATGGCGACAGTGCAGATG	2475
Qy	713	AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732
Dd	2476	GACCAAGTGGAGGGCTCGCATTCCTGGGCCGGAAGATAGCTTCATGACCTTAGCCGA	2535
Qy	733	ValGlyIleHisGlyTrpSerTyrGlnGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752
Dd	2536	CTTGCCATCCATGGCTGGCTCTACGGGGCTTCCTGCTCATGATGGGCTAATCACAAG	2595
Qy	753	SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp	772
Dd	2596	CCCCAGGTTCAAGTGGGCAATCGGGGCGCCCGTCACCGTGGATGGCTACAGAC	2655
Qy	773	ThrGlyTyrThrGluArgTyrMetGlnLysProAspGlnAsnGlnGlyTyrTyrLeu	792
Dd	2656	ACGAGGTACATGAGCCCTCATGAGACCTCCCTGAAACACACACACGCTATGAGCGC	2715
Qy	793	GlySerValAlaMetGlnAlaGlnLysPheProSerGlyProAsnArgLeuLeuLeu	812
Dd	2716	GGTTCCGAGGCCCGACAGTGAAGAGCTGCCAATAGACCCCAACGCTTGCTTATGCTC	2775
Qy	813	HisGlyPheLeuAsnArgIleAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu	832
Dd	2776	CACGCTTCCTCGAGCAAAACGTCACCTTTTTCACACAAACTCTCTGCTCCCACTG	2835
Qy	833	ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGlnArgHisSerIleArg	852
Dd	2836	ATCCGACGAGGAAACCTTACACAGCTCCGAGATTAACCCAAAGAAAGACAGATTTGCG	2895
Qy	853	ValProGluSerGlyGlnHisTyrGluLeuHisLeuLeuHisTyrLeuGlnGluAsnLeu	872
Dd	2896	TGCCCGAGTGGGCGAGCACTATGAAGACAGTTGCTCACTTTCTACAGGAATACCTC	2955
RESULT 18			
ABK83333			
ID	ABK83333	standard; cDNA; 4302 BP.	
XX	ABK83333:		
AC	12-AUG-2002	First entry)	
DT	cdna	encoding human DPR-2 splice variant #1.	
XX	Human; serine protease; dipeptidyl peptidase IV-related protein; DPR;		
KW			

KM DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KM diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KM heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KM ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KM dyskinesia; reproductive disorder; inflammatory disorder;
 KM metabolic disorder; gene; ss.
 OS Homo sapiens.
 PN MO2002J1134-A2.
 PD 18-APR-2002.
 PF 12-OCT-2001; 2001MO-US31874.
 PR 12-OCT-2000; 2000US-240117P.
 PA (FERR) FERRING BV.
 PI Q1 S, Akinsanya KO, Riviere PJ, Junien J;
 DR WPI; 2002-444178/47.
 DR P-PSDB; AB661602.
 XX
 PS New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 XX
 XX Disclosure; Page 78-79; 113pp: English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bllima, Parkinson's disease, acute heart failure, hypertension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
 XX
 XX Sequence 4302 BP; 923 A; 1350 C; 1221 G; 808 T; 0 other:
 SO
 Alignment Scores:
 Pred. No.: 8,66e-283 Length: 4302
 Score: 2870.00 Matches: 517
 Percent Similarity: 77.50% Conservative: 134
 Best Local Similarity: 61.55% Mismatches: 187
 Query Match: 61.06% Indels: 2
 DB: 24 Gaps: 2
 US-10-070-464-1 (1-882) x ABK83333 (1-4302)
 Oy 35 PhetyrValGluArgTyrSerTrpSerGlnLeuLysLysLeuAlaAspThrArgLys 54
 Db 436 TTCAGGTGAGAGGACGCTGCGGAGCGGCTCGGAGCATCACCGCGGAGGAG 495
 Oy 55 TyrHisGlyTyrMetAlaLysAlaProHisAspPheMetPheValLysArgAsp 74
 Db 496 TACGCGGCGCATTCGTCACAAAGGCGGCCACGACCTTCCAGTTTGCCAAACAGCAT 555
 Oy 75 ProAspGlyProHisSerAspArgIleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94
 Db 556 GAGTGTGGGCGCCGACCTCCGAGCGGCTCTACTACTGGAATGCCATATGAGAGCGGAG 615
 Oy 95 AsnThrPheTyrSerGluIleProLysThrIleAsnArgAlaValLeuMetLeu 114
 Db 616 AACCTCCCTCTACTGTGAGATTCCCAAGAGGTCGCGAAGAGGCTGCTGCTCTG 675

Oy 115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
 Db 676 TCCGGAAGCAGATGCTGATGATTCATCCAGGCCACGCCACCATGGGCTACTCTCGG 735
 Oy 135 GluGluGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
 Db 736 GAGGAGGAGCTGCTGAGGAGCAGGAAACGCTGGGGGCTTCGATCACCTCTACGAC 795
 Oy 155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
 Db 796 TTCACAGCGAGAGTGCTGCTCTCTCCAGGCCAGCAACACCTCTTCACCTGCGCG 855
 Oy 175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
 Db 856 GACGCGCGCAAGAACGCGCTTCATGCTGCTCCCTATGAACCGCTGGAATACAGACCCAG 915
 Oy 195 CysProAsnIleArgMetAspProLysLeuGlyProAlaAspProAspTyrIleAlaPhe 214
 Db 916 TGCTCAGGCGCCCGATGAGACCCCAAAATGCTGCTGCGACCTCTCTCTCTCTC 975
 Oy 215 IleHisSerAsnAspIleTrpIleSerAsnIleValIleThrArgGluGluArgArgLeuThr 234
 Db 976 ATCATATAACAGCAGCTGTGGTGCCCAACATCCAGACAGGAGGAGCGGCGCTGACC 1035
 Oy 235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254
 Db 1036 TTCGCGCCCAAGGTTTATTCATATCTCTCGATATGACCCCAAGTCTGCGGTGCGCAC 1095
 Oy 255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTyrProCysProLysAlaGlu 274
 Db 1096 TTCCTCATACAGGAAGATTGCGACCGCTTCACTGCTGCTGCTGCTGCTGCTGCTG 1155
 Oy 275 ThrThrProSerGlyGly---LysIleLeuArgIleLeuTyrGluGluAsnAspLysSer 293
 Db 1156 TGGAGAGCTTCAGAGGCGCTTCACAGCGCTGCAATCTGTTGAGAGGATGATGATGCC 1215
 Oy 294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
 Db 1216 GAGTGGAGGATTCATTCACGCTCCCTCTCTCTGCTAGAGAAAGAGACGAGCTCGAT 1275
 Oy 314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet 333
 Db 1276 CGGTACCCGACAGGAGGAGCAGCAAGATCCCAAGATTGCTGTTGAACGTGCGATTCAG 1335
 Oy 334 IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
 Db 1336 ACTGACAGCCAGGCGCAAGATGCTCGACCCAGAGAGAGAGGAGTGTCCACCTTCAGC 1395
 Oy 354 IleLeuPheGluGluValGluTyrIleAlaArgAlaGlyThrProGluGlyLysTyr 373
 Db 1396 TCGCTGTTCGGAAGGTGAGTACATGCCAGGCGGGGTGAGCCGGATGCGCAATATC 1455
 Oy 374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro 393
 Db 1456 GCGTGGGCAATGCTCTGAGACCGGCCCCAGCAGTGGCTCGAGTCTCTCTCTCTCC 1515
 Oy 394 GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal 413
 Db 1516 GCCCTGTTCATCCGAGACAGCAAGATGAGAGGAGGAGGCTAGCCTTGCAGAGCTGTC 1575
 Oy 414 ProAspSerValThrProLeuIleIleLeuGluGluThrTrpAspIleTyrIleAsnIle 433
 Db 1576 CCCAGAGATGTCAGCGCTATGCTGTGACAGAGAGGATCACCAACGCTGTGATCAATGTT 1635
 Oy 434 HisAspIlePheHisValPheProGlnSerHis--GluGluGluIleGluPheIlePhe 452
 Db 1636 CATACATCTCTTATCTCTCCCAATCAAGAGGAGGAGGAGGAGCTGCTCTCTCCGC 1695
 Oy 453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
 Db 1696 GCCATGATGCAAGACCGGCTTGCCTATTTGACAAAGTACACGCGCTTTTAAATTC 1755

OY	473	SeLysTrLyLysATGSerSergLYLLeuProAlaProSerAspPheLysGyrProle	492
Db	1736	CAGGCGTACGATTGGAGTGAACCCCTTACGCCCGGGGAAGATGAATTAAAGTCCCATTT	1815
OY	493	LysGLuGLuIleAlaIleThrSerGLyGLuTrpGLuValLeuGLyArgHisGLySerAsn	512
Db	1816	AAGGAAAGATTTGCTCTTGACCAGCGGGAATGGAGGATTTTGGCCAGCCAGCGCTCCAAAG	1875
OY	513	IleGLuValAspRgiValAlaArgArgLeuValTyrPheGLuGLyThrLysAspSerProleu	532
Db	1876	ATCTGGGTCAATGAGGAGACCAACACTGGTACTTCCAGGCAACGAGACAGCGCGCTG	1933
OY	533	GLuHisHisLeuTyrValAlaSerTyrValAsnProGLyGLuValThrArgLeuThrAsp	552
Db	1936	GAGCAACCACTCTACGATGGTACGATAGAGCGCGGGAAGATGCTACGCCCTCACAG	1995
OY	553	ArgGLyTyrSerHisSerCysCysIleSerGLuHisCysAspPheIleSerLysTyr	572
Db	1996	CCCGCTTCTCCATCTACTCTCTCCATAGCAACACTTGATGTTGTCGACCACTAC	2055
OY	573	SerAsnGLyAsnProHisCysValSerLeuTyrLysLeuSerSerProGLuAsp	592
Db	2056	AGCAGCGTACACGCGCGCGCTGCTACAGTCTACAACTAGAGCGGCCGACACAGCAC	2115
OY	593	ProThrCysLysThrLysGLuPheTrpAlaThrIleLeuAspSerAlaLysProLeuPro	612
Db	2116	CCCCGCAACAAGCAGCCGCCCTCTGGGCTAGCATGATGAGGACACAGCTGCCCCCG	2175
OY	613	AspTyrThrProProGLuIlePheSerPheGLuSerThrThcGLyPheThrLeuArgly	632
Db	2176	GATTATGTCTCTCCAGAGATCTTCATTCTCACACCGCTCGGATGCGGCTTACGCG	2233
OY	633	MetLeuTyrLysProHisAspLeuGLuProGLyLysLysTyrProThrValLeuPheIle	652
Db	2236	ATGATCTACAAGCCCCCAGCGCTTGGACCCAGGAAAGACAGCCCACTCTCTTTGTA	2295
OY	653	TyrGLyLysProGLuValAlaGLuLeuValAsnAsnArgPheLysGLyValLysTyrPheArg	672
Db	2296	TATGGAGGCCCCAGGTGACGTGTGTAAATACTCTTCAAAGCAATCAAGTACTTGGCG	2355
OY	673	LeuAsnThrLeuAlaSerLeuGLyTyrValValValIleAspAsnArgLysCys	692
Db	2356	CTCAACACACTGAGGCTCCCTGGGCTACGCGGTGTGATTGACGAGGCGCTCTGT	2415
OY	693	HisArgGLyLeuLysPheGLuGLyAlaPheLysTyrLysMetGLyIleLeuIleLysP	712
Db	2416	CAGCGAGGCTTCGGTTCCAGAGGGGCCCTGAAACCAATATGGCCAGGTGAGATCGAG	2475
OY	713	AspGLuValGLuGLyLeuGLuIleTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732
Db	2476	GACCAAGTGGAGGGCGTGCAGATTCGTGTGGCGAGAGAATAGTTCATGACCTGAGCGGA	2533
OY	733	ValGLyIleHisGLyTrpSerTyrGLyIleTyrLeuSerLeuMetAlaLeuMetGLuArg	752
Db	2536	GTTGGCAATCCATGGCTGTGCTCTACGGGGCTTCCTCTCGCTCATGGGCTAATTCACAG	2595
OY	753	SerAspIlePheArgValAlaIleAlaGLyAlaProValThrLeuThrPhePheLysP	772
Db	2596	CCCCAGGTTCACAGGTGGCCATGCGGGTCCCGGCTACCGCTCTGATGGCTACGAC	2655
OY	773	ThrGLyTyrThrGLuArgTyrMetGLyHisProAspIleAsnGLuGLuIleTyrTyrLeu	792
Db	2656	ACAGGCTACACTGAGCGCTCATGTGAAGTCTCGAGAACACACAGCAGCGTATGAGGGG	2715
OY	793	GlySerValAlaMetGLuIleGLuLysPheProSerGLuProAsnArgLeuLeuLeu	812
Db	2716	GGTTCCCGGCGCTCGCACGTGGAAACACTGCCAATAAGAGCCCAACCGCTTGTATCTC	2775
OY	813	HisGLyPheLeuAspGLuAsnValHisPheAlaHisThrSerIleLeuSerPheLeu	832
Db	2776	CACGGCTTCGAGCAAGAAAGTGCACATTTTCCACACAACATCTCTGTTCCCAACTG	2833
OY	833	ValArgAlaGLyLysProTyrAspLeuGLuIleTyrProGLuIleArgHisSerLeuArg	852

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Db      2836 ATCCGACGAGGAAACCTTACACAGCTCCAGATATTACCACGAGAGACAGACTTTTGC 2895
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Oy      853 ValProGluSerGlyGluHisTyrGluLeuHisLeuLeuHisTyrGluGlnAsnLeu 872
      |||||
Db      2896 TGCCCCGAGTGGGCGACGACACTGATGAAGTCACGCTTCTGCTACACTTCTACAGGAAATACCTC 2955
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RESULT 19
AAD38954
ID      AAD38954 standard; cDNA; 3024 BP.
XX
XX      AAD38954;
AC
XX
XX      23-SEP-2002 (first entry)
DE
XX
XX      Human dipeptidyl peptidase 9 (DPP9) cDNA.
DE
XX
XX      Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW      autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW      graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW      antiviral; enzyme; gene; ss.
XX
XX      Homo sapiens.
OS
XX
XX      Key
FH      Location/Qualifiers
FT      CDS
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      /transl_except= (pos: 1120..1122, aa:Gln)
      /note= "CDS does not include start codon"
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XX
XX      02-MAY-2002.
PD
XX
XX      29-OCT-2001; 2001WO-AU01388.
PF
XX
XX      27-OCT-2000; 2000AU-0001078.
PR
XX
XX      (UNSY ) UNIV SYDNEY.
PA
XX
XX      Abbott CA, Gorrell MD;
PI
XX
XX      WPI: 2002-454646/48.
DR
XX
XX      P-PSDB; AAE24168.
XX
XX      New dipeptidyl peptidase (DPP) peptidases, useful for screening
PT      inhibitors of DPP catalytic activity, which may be employed to treat
PT      e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT      rejection and HIV infection -
XX
XX      PS      Example; Fig 4; 91pp; English.
XX
XX      The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC      polynucleotides encoding such proteins. The DPP peptides are useful for
CC      screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC      for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC      rejection and HIV (human immuno deficiency virus) infection. The present
CC      sequence is human DPP9 cDNA.
XX
XX      SQ      Sequence 3024 BP; 624 A; 973 C; 875 G; 552 T; 0 other;
Alignment Scores:
Pred. No.:      2.63e-282      Length:      3024
Score:      2863.00      Matches:      516
Percent Similarity:      77.38%      Conservative:      134
Best Local Similarity:      61.43%      Mismatches:      188
Query Match:      60.91%      Indels:      2
DB:      24      Gaps:      2
US-10-070-464-1 (1-862) x AAD38954 (1-3024)

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Db	1468	GCCTGTTTCATCCCGACACAGAAATGAGGAGCACCGGCTAGCCCTCCACAGCTGTC	1527
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Db	1528	CCGAGAAATGTCACGCGGTATGTGTGTGTACAGAGAGTCCACAACTCTGTGATCATGT	1587
Qy	434	HisAspIlePheHisValPheProGlnSerHis--GluGluGluIleGluPheIlePhe	452
Db	1588	CATGACATCTTCTATCCCTTCCCCCAATCCAGAGGAGAGACAGCACTGCTGTTTCCGC	1647
Qy	453	AlaSerGluCysLysThrGlyPheThrGlnHisLeuTyrLysIleThrSerIleLeuLysGlu	472
Db	1648	GCCATGATGCAAGACCGGCTTCTGCATTTGTACAAAGTCCACCGCTTTAAATCC	1707
Qy	473	SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerSerPheLysCysProIle	492
Db	1708	CAGGCGTACATGTGAGTGAAGCCCTTACGCCCGGGGAAGATGAATTAAAGTCCCAT	1767
Qy	493	LysGluGluIleAlaIleThrSerGlyGlyTrpGluValLeuGlyValGlnHisGlySerAsn	512
Db	1768	AAGAAAGATTTGCTGTACACAGCGGTGATGGAGATTGTCGAGGACACGCGTCCAG	1822
Qy	513	IleGlnValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu	532
Db	1828	ATCTGGGTCATGTAGGAGACCAAGCTGTCTACTCCAGGCGCCCAAGACACCGCGCTG	1887
Qy	533	GluHisHisLeuTyrValAlaSerTyrValAsnProGluValIleThrArgLeuThrAsp	552
Db	1888	GAGCAACACCTCTACGTGTGTACGTAAGAGCGCGGCGGAGATGATTAAGTCCACACG	1947
Qy	553	ArgGlyTyrSerHisSerCysCysIleSerGlnHisCysAspPheIleSerLysTyr	572
Db	1948	CCCGGCTTCTCCATAGCTGTCTCCATGAGCAGACATCGATGTCAGAGCCATAC	2007
Qy	573	SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGlnAspAsp	592
Db	2008	AGCAGCGTGAGACGCGCGCTGTGTCTACAGTACAGCTGAGCGCGCCGACGACGAC	2067
Qy	593	ProThrCysLysThrLysGluPheThrAlaThrIleLeuAspSerIleGlyProLeuPro	612
Db	2068	CCCCGACACAGACGCCCCGCTTGTGGCTAGCATGTATGAGGACACGACTGCCCGCG	2122
Qy	613	AspTyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly	632
Db	2128	GATTATGTCTCCAGAGATCTTCCATATTCACACGCGCTCGGATGGCGCTACAGCG	2187
Qy	633	MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle	652
Db	2188	ATGATCTACAAAGCCCCACGCGCTTGCAGCCAGGCAAGACGCCACCGCTCTTTGTA	2247
Qy	653	TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyLysLysTyrPheArg	672
Db	2248	TATGAGAGCCCCAGGTCAGCTGTGTGAATATCTCTTCAAGGACATCAAGTACTTGGC	2307
Qy	673	LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgLysCys	692
Db	2308	CTCAACACACTGGGCTCCCGGGCTACGCCGTGTGTGATTGTACGGCAGGGCTCTCT	2367
Qy	693	HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp	712
Db	2368	CAGCGAGGGCTTCGTTCTGAAAGGGGCGCTGAAAAACCAATGGCCAGCTGAGATCGAG	2422
Qy	713	AspGlnValGluGlyLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732
Db	2428	GACCAAGTGGAGGGCTGTGACAGTTTCGTGGCCGAGAACTATGCTCTTCTTCCACTTGAGCGCA	2487
Qy	733	ValGlyIleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2488	GTTCCCATCATGCGCTGTGTCTTACAGGGGCGCTTCTTCGCTCATGTGGGCTAATCCACAAG	2542
Qy	753	SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuThrPilePheTyrAsp	772

Db 2348 CCCCAGGTGTCAAGTGGCCATCGCGGTGCCCCGCTACCGCTGTGATGCGCTACGAC 2607
 QY 773 ThrglythrThrgluArgTyrMetGlyHisProaspGlnasnGlnGlnGlyTyrTyrLeu 792
 Db 2608 ACAGGGTACACTGAGCGCTACATGAGCTCCCTGAGAACACACGACGCGGTATGAGCGC 2667
 QY 793 GlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeu 812
 Db 2668 GGTTCGCGGCGCTGCACAGTGGAGAGCTGCCCAATGAGCCCAACCGCTTCTTATCCTC 2727
 QY 813 HisIleGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
 Db 2728 CACGGCTTCCGTGACGAAACGTCACCTTTTCCACACAACTTCTGCTCTCCCACTG 2787
 QY 833 ValArgAlaGlyLysProTyrAspLeuGlnIleTyrProGlnGlnIuArgHisSerIleArg 852
 Db 2788 ATCCGACAGGGAACCTTACCACTCCAGATCTACCCCAACGAGACACAGATATTCGC 2847
 QY 853 ValProGluSerGlyGluHisTyrGluLeuHisLeuHisTyrLeuGlnGluAsnLeu 872
 Db 2848 TGCCCCGAGTGGCGGACACTATGAGTACAGTCTTACTGCACTTCTTACAGAAATACCTC 2907
 RESULT 20
 AAD38957 standard; DNA; 2495 BP.
 ID AAD38957
 AC AAD38957;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human dipeptidyl peptidase 4 (DPP4)-like 2 DNA.
 XX
 KM Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
 KM autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
 KM graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
 KM antiviral; enzyme; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT /product= "Human DPP4-like 2 protein"
 FT /transl_except= (pos: 703..705, aa:Gln)
 FT /note= "CDS does not include start codon"
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 XX
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 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001MO-AU01388.
 XX
 PR 27-OCT-2000; 2000AU-0001078.
 XX
 PA (UNSY) UNIV SYDNEY.
 XX
 PI Abbott CA, Gorrell MD;
 XX
 DR WPI; 2002-454646/48.
 DR P-PSDB; AAE24171.
 XX
 PT New dipeptidyl peptidase (DPP) peptidases, useful for screening
 PT inhibitors of DPP catalytic activity, which may be employed to treat
 PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
 PT rejection and HIV infection -
 XX
 PS Disclosure: Page 86-88; 91pp; English.
 XX
 CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
 CC polynucleotides encoding such proteins. The DPP peptidases are useful for
 CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
 CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft

CC rejection and HIV (human immuno deficiency virus) infection. The present
 CC sequence is human DPP4-like 2 DNA.
 XX
 SQ Sequence 2495 BP; 535 A; 783 C; 696 G; 481 T; 0 other;

Alignment Scores:

Pred. No.:	1,44e-279	Length:	2495
Score:	2835.00	Matches:	512
Percent Similarity:	77.47%	Conservative:	131
Best local Similarity:	61.69%	Mismatches:	185
Query Match:	60.32%	Indels:	2
DB:	24	Gaps:	2

US-10-070-464-1 (1-882) x AAD38957 (1-2495)

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 Db 1 CTCCGAGCATCATCAACCGCAGCGGCAAGTACCTCGGGCTCATTTGTCAACCAAGCGGCC 60
 QY 65 HisAspPheMetPheValLysArgAsnAspProaspGlyProHisSerAspArgIleTyr 84
 Db 61 CACGACTTCCAGTTTGTGCCAACAACGAGATGAGTGGGCCCTCCACCGCTCTAC 120
 QY 85 TyrLeuAlaMetSerGlyGluAsnArgLysAsnThrLeuPheTyrSerGluIleProLys 104
 Db 121 TACCTGGGAATGCCATATGCGAGCGGAGAACTCCCTCTACTCTGAGATTCCCAAG 180
 QY 105 ThrIleAsnArgAlaValAlaValMetLeuSerTyrLysProLeuLeuAspLeuPheGln 124
 Db 181 AAGTCCGGAAGAGAGGCTGTGCTGCTCTGCTGAGAGACAGATGTGATTCATTTCCAG 240
 QY 125 AlaThrLeuAspTyrGlyMetTyrSerArgGluGluLeuLeuAspGluArgLysArg 144
 Db 241 GCCACGCGCCCAACATGAGGGGTCTACTCTCGGAGAGAGAGCTGCTGAGGAGCGGAAACGC 300
 QY 145 IleGlyThrValGlyIleAlaSerTyrAspTyrHisGlnGlySerGlyThrPheLeuPhe 164
 Db 301 CTGGGGCTTCTGGCATCACCCTCTACGACTTCCACACGAGAGATGGCTCTTCTCTTC 360
 QY 165 GlnAlaGlySerGlyIleTyrHisValLysAspGlyGlyProGlnGlyPheThrGlnGln 184
 Db 361 CAGCCACAGACAGCCCTCTTCTCCTCCGCGCGCGGCAAGACGCTTCATGTGCTCC 420
 QY 185 ProLeuArgProAsnLeuValGluThrSerCysProAsnIleArgMetAspProLysLeu 204
 Db 421 CGTATGAACCCGCTGCAATCAACAGCACGCTCAGGGCCCGGATGGAGCCCAAAATC 480
 QY 205 CysProAlaAspProAspTyrPheAlaPheIleHisSerAsnAspIleTyrPheSerAsn 224
 Db 481 TGCCCTGCCGACCTGCTCTCTCTTCTTCAACAATTAACACGACCTGTGGTGGCCAAC 540
 QY 225 IleValThrArgGluGluArgArgLeuThrTyrValHisAsnGlnLeuAlaAsnMetGlu 244
 Db 541 ATCGAGACAGGCGGAGCGGCGCTGCTTCTGCGCACCAAGTTTATTCAAAATGCTCG 600
 QY 245 GluAspAlaArgSerAlaGlyValAlaThrPheValLeuGlnGluGluPheAspArgTyr 264
 Db 601 GATGACCCCAAGTGTGGGGGTGGCGCACCTCTCATACGAGAAGTTCGACCGCTTC 660
 QY 265 SerGlyTyrTrpTyrCysProLysAlaGluThrThrProSerGlyGly--LysIleLeu 283
 Db 661 ACTGCGTACTGTGCTGCTGCCACACCTCTCGGAGAGTTTCAGAGCCCTCAACACGCTG 720
 QY 284 ArgIleLeuTyrGluGluAsnAspGluSerGluValGluIleIleHisValThrSerPro 303
 Db 721 CGAATCTGTATGAGAGTGTGATGATGAGGTGAGGTGATGATGATGATGATGATGATG 780
 QY 304 MetLeuGluThrArgArgAlaAspSerPheArgTyrProLysThrGlyThrAlaAsnPro 323
 Db 781 GCGCTAAGAGAAG 840
 QY 324 LysValThrPheLysMetSerGluIleMetIleAspAlaGluGlyArgIleIleAspVal 343
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Db	841	AAGATGGCTTGAACATGCGCTGATGTTCCAGACTGACAGCCAGGACAGATGGTCTGCACC	900
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Db	901	CAGAGAGAGGAGCTGGTGGCAGCCCTTACCTGCTGCCAGAGTGGAGACTATGCC	960
Oy	364	ARGALAGLTPRTPROGLUGLYSTYRALATPSERILEULEUASPARSERGLN	383
Db	961	AGGGCCGGGTGGACCCGGGATGGCAATACGCTGGGCGATCTTCTTGACGGGCCAG	1020
Oy	384	THARGLUEINILEVLEULEISERPROGLUEPHELEPROVALGLUASPARVAL	403
Db	1021	CAGTGGCTCCAGTCCGTCCTCTCCGCCGGCGCTGTTCATCCGACGACAGAGANTAG	1080
Oy	404	METGLUARGGLUEULEGLUSERVALPROASPERVALTHPROLEULEILEYR	423
Db	1081	GAGCAGGCGCTAGGCTCTGCGACAGCTGTCCGACAGAAATGTCACACCTATGGGTGAC	1140
Oy	424	GLUGLUTHRASHRIETPRILEANILEHISASPLEPHEHISVALPHEPROGLSER	443
Db	1141	GAGAGGTCACACAGCTGTGATCATATGTTCATGACATTTTATCCCTTCCCAATCA	1200
Oy	444	HLIS--GLUGLUGLUILEGIUPEHILEPHEALASERGLUCYSTHGLYPHEARHIS	462
Db	1201	GAGGAGAGGAGCAGAGCTCTCTTCTCCCGCCAAATGATGACAAACGGCTTCTGCAT	1260
Oy	463	LEUTYRYSILETHRSERILEULYSGLUSERLYSTYRYSALRSERSEGLYGLU	482
Db	1261	TTGTATCAAAAGTACCCCGCTTTAAATATCCAGAGCTACGATTGGAGTGAGCCCTTACG	1320
Oy	483	PROHLAPROSERASPERHLYSCYSPROILLELYSGLUGLUIALALETHSERGLYU	502
Db	1321	CCCGGAGAGATGAAATTAGTCCCATTAAGGAAGAAATGTGCTGACACAGCGCTAA	1380
Oy	503	TRPGLUALLEUGLYARHISGLYSERANILEGNVALASGLIVALARGARLEUAL	522
Db	1381	TGGGAGGTTTTGGGAGAGCAGCGGCTCCAGATCTGGGTAAAGAGAACCAAGTGGTG	1440
Oy	523	TYRPHIEGLUTYRILYASPSERPROLEUGLUNHSHISLEUTYRVALVASETYRVAL	542
Db	1441	TACTTCCAGGCGACCAAGACGAGCGGCTGGAGACACCTCTACGTGTGAGTATAG	1500
Oy	543	ASNPROGLYGLUVALTHRARGLEUTHRAPRARGLYTYRSEHISSERCYSGLISER	562
Db	1501	CGGCGCGGAGATCGTACCCCTCACACCGCGGCTTCCCAATGCTGTCCATGAGC	1560
Oy	563	GLNHISYASPARPHEHILESERLYSYRSEANGLYASPROHISCYVALSER	582
Db	1561	CAGAACTTCGACATGTTCTGTCACCACTACAGCAGCGTAGACACCCGCTGCTGCAC	1620
Oy	583	LEUTYRYSLEUSERSERPROGLUASPARPROTHCYSLYSTHLYSGLUPHETRALA	602
Db	1621	GTCATCAAGCTGAGCGGCGCCGACGACGACCCCTCACAAACAGCCCGGCTTGCGCT	1680
Oy	603	THRILELEUASPSERALAGLYPROLEUPROASPTYRTHPROPROGLUIEPHERPHE	622
Db	1681	AGCATGATGAGGAGGACCACTGCCCGCGAATATGTTCTCCAGAGATCTTCATATTG	1740
Oy	623	GLUSERTHRTGLYPHEHILEUTYRGLYMETLEUTYRGLYPROHISASPERGLU	642
Db	1741	CACACGGCGCTCGATGTGGCGGCTCTACGGCATGATTTACAAACCCCAAGCCTTGACGA	1800
Oy	643	GLYLYSLYSTYRPROTHVALLEUPHEILETYRGLYPROGLIVALGLINLEUVALSN	662
Db	1801	GGGAAGAAGCACCCACCGTCTCTTTATATATGAGGCCCCCAGTAGGTGGTGAAT	1860
Oy	663	ASPARGLPELYSGLYVALYSTYRPHIARGLEUASNTHLEUALISERLEUGLYTYVAL	682
Db	1861	AACCTCTTCAAGGACATCAAGACTTGGCGCTCAACACACTGGCTCCCTGGGCTACGCC	1920
Oy	683	VALVALVALILEASPARASPARGLYSERYSHISARGLYLEULYRPHIEGLUYALAE	702
Db	1921	GTGGTGTATGACGGCGAGGGCTCTCTGTCACGAGGGCTTCGGTGTGAAAGGGCCCTG	1980

QY	703	LYSTYLRLVSMETGLVGHINILLEGUILLLEASAPGILNVALGILVLENGILTYRLEUHLA	722		
Db	1961	AAAAACCAATGAGGCCAGGAGTGAGATCGAGACACAGGTGAGAGGCGCTGACAGTTCTGGCC	2040		
QY	723	SEARFGTYRASPHEILAEAPLEASPARGVALGILYLEHISGLTYRSPERTYRGLYGLY	742		
Db	2041	GAGAAAGTATGGCTTCATCGACCTGAGCCGAGTTGCCATTCATGGCTGAGTCAGCGGGCC	2100		
QY	743	TYRLEUSERLEUWELALAEUWETGILNARGSERASPILREHARGVALALALLENLAELGLY	762		
Db	2101	TTTCCTCTCCCTCATGGGGGCTAAATCCACAAAGCCCAAGGTGTTCAGAGTGCGCCATCCCGGGT	2160		
QY	763	ALAPROVALTHIRLEUTRPILPEHETRYRASPTRHGLTYRTHGLUARGTYRMETGLYHIS	782		
Db	2161	GCCCCGCTCACCCGCTGTGATGGCTTACGACACAGGCTACACTGAGCGCTACATGAGCACTG	2220		
QY	783	PROASPGILNANGILNGILTYRTRYRLEUGLYSERVALALAMETGLNALAGLULSPHE	802		
Db	2221	CCGTGAGAACAACACAGCAGCGCTATGAGAGCGGGTTCCTCGGCTGCACGTGGAGAAAGCTG	2280		
QY	803	PROSERGILUPROASNAHGLEULEUENLEUHLHISGLYPHELEUASPGILNANVALHISHE	822		
Db	2261	CCCAATGAGCCCAACCCCTGCTTATTCCTCCACAGGCTTCTGTGACGAAAACTGCACCTT	2340		
QY	823	ALAHSTRSERILELEULEUSERPHELEUVALJARGALAGLYLVSPTOTYRASPLEUGIN	842		
Db	2341	TTTCCACACAAACTCTCTCTGCTCCCAACTGATATCTCGAGCAGGGAACCTTACCAAGCTCAG	2400		
QY	843	ILEYTRPROGLINGUARHISSERILEARGVALPROGLINSERGLYGLINHISTYRGLULEU	862		
Db	2401	ATCTAACCCCAACGAGACACAGATTCGCTGCCCGAGTCCGGAGACAGCATATGAAGTC	2460		
QY	863	HISTLEULEHISTYRLEUGINGILNANLEU	872		
Db	2461	ACGTTACTGCATTTCTACAGAAATACCTTC	2490		
RESULT 21					
ID	AAD38955				
XX	AAD38955 standard; cDNA; 3287 BP.				
AC	AAD38955;				
XX					
DT	23-SEP-2002 (first entry)				
XX					
DE	Alternative version of murine dipeptidyl peptidase 9 (DPP9) cDNA.				
XX					
KW	Murine: dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection;				
KW	human: immuno deficiency virus; graft rejection; cytostatic; autoimmunity;				
KW	type II diabetes; antidiabetic; antiinflammatory; immunosuppressive;				
KW	antiviral; enzyme; gene; ss.				
XX					
OS	Mus sp.				
XX					
PH	Key				
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XX					
XX	27-OCT-2000: 2000AU-0001078.				
XX					
PA	(UNSY) UNIV SYDNEY.				
XX					
PI	Abdolt CA, Gorrell MD;				

DR WPI: 2002-45466/48.
DR P-PSDB: AAE24169.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
PS Disclosure: Page 67-70; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immunodeficiency virus) infection. The present
CC sequence is an alternative version of murine DPP cDNA.
CC Note: This sequence is stated to be the same as that shown as
CC SEQ ID NO: 3 in figure 9 of the specification. However these sequences
CC differ.
XX
SO Sequence 3287 BP; 744 A; 970 C; 877 G; 696 T; 0 other;

Alignment Scores:
Pred. No.: 3,52e-279 Length: 3287
Score: 2833.00 Matches: 511
Percent Similarity: 76.79% Conservative: 134
Best Local Similarity: 60.83% Mismatches: 193
Query Match: 60.28% Indels: 2
DB: Gaps: 2

US-10-070-464-1 (1-882) x AAD38955 (1-3287)

QY 35 PheTyrValGluArgTyrSerGlnLeuPheLysLeuLeuAlaAspThrArgLys 54
DB 88 TTCTGTGTGCGAGACGACCTCTGGATGGCTGGCTGACATTATCCAGCGACGCGACG 147
QY 55 TyrHisGlyTyrMetMetAlaLysAlaProHisAspPheMetPheValLysArgAsnAsp 74
DB 148 TCTCGGAGCCTATTGTGACGAGGCGCCCGACGACCTTCCAGTTGTGACAGACCTGAC 207
QY 75 ProAspGlyProHisSerAspArgLleTyrTyrLeuAlaMetSerGlyGluAsnArgLys 94
DB 208 GAGTGTGGCCCGCCACTCTACCGTCTATTACCTCGGAATGCTTACGCGACGCGTAG 267
QY 95 AsnThrLeuPheTyrSerGlnLeuPheLysThrIleAsnArgAlaValIleuMetLeu 114
DB 268 AACCCCTCTCTCTCTCCGATCCCAAGAACTCCGAGAGAGAGCGCTCTGCTGCTG 327
QY 115 SerTyrLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
DB 328 TCTCGAAGCAGATGTGACACCTTCACGCGCACACCCACCATGTGCTACTCCCGA 387
QY 135 GluGluGluLeuLeuArgGluArgLysArgLleGlyThrValGlyIleAlaSerTyrAsp 154
DB 388 GAGAGAGAGCTACGCGGAGCGAGCGCTGGCGCTTCGGAATCACTCTTATGAC 447
QY 155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyIleTyrHisValLys 174
DB 448 TTCCACAGTAGAGCGGCTCTCTCTCCAGGCGAGCATATACCTGTTCACAGG 507
QY 175 AspGlyLysProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
DB 508 GATGCGTCAAGAAATGCTTATGCTCCCGCATGAAGCAGTCGAGATCAACAGCTAG 567
QY 195 CysProAsnIleArgMetAspProLysLeuLysProAlaAspProAspThrIleAlaPhe 214
DB 568 TGTCTGTGGCCAGCAGTACGAGCCCAAAATCTGCCCCGACAGCCTGCTTTTCTCCTC 627
QY 215 IleHisSerAsnAspIleTyrPheLysSerAsnIleValThrArgGluGluArgArgLeuThr 234
DB 628 ATCAACAACAGTATCTGTGTGTGCGCAACATCGAGACTGGGAGAGAAAGCGGCTCACC 687
QY 235 TyrValHisAsnGluLeuAlaAsnMetGluGluAspAlaArgSerAlaGlyValAlaThr 254

DB 688 TTCTGTACACGAGGCTTCAGCTGCTGCTGACATCCCAATCAGACGCGTCCACC 747
QY 255 PheValLeuGlnGluGluPheAspArgTyrSerGlyTyrTrpTyrProLysAlaGlu 274
DB 748 TTGTTCATCCAGAGAGGAGTTCAGCGCTTCAGTGGTGCTGTGTGCTCCACGGCTCT 807
QY 275 ThrThrProSerGlyGlyLysIleLeuArgLleLeuTyrGluGluAsnAspGluSer 293
DB 808 TGGAGAGCTTCGGAAGGCTTCACAGCAGCTCCGATCTATATAGAGAGAGAGACTCT 867
QY 294 GluValGluIleIleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
DB 868 GAATGTAGAGCATTCATGTCTCCCTCCCGCTCGAGAGAGAGAGAGAGAGAGAGAG 927
QY 314 ArgTyrProLysThrGlyThrAlaAspProLysValThrPheLysMetSerGluIleMet 333
DB 928 CGCTACCCAGAGACAGCAGCAGACAGACCCAGATTCCTGAGAGCTGGCTGACCTCAG 987
QY 334 IleAspAlaGluGluArgLleIleAspValIleAspLysGluLeuIleGlnProPheGlu 353
DB 988 ACGGACCATCAGGCGCAAAATCTGTCAAGCTCGCAGAGAGAGAGAGAGAGAGAGAG 1047
QY 354 IleLeuPheGluGluGluValGluTyrIleAlaArgAlaGlyTyrProGluGlyLysTyr 373
DB 1048 TCCCTTTTCCCAAGAGAGAGATCATCGCCGCGCTGCTGTGACAGCGAGCAAAATAT 1107
QY 374 AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValIleIleSerPro 393
DB 1108 GCTGTGGCCATGTCTCGAGACCGTCCAGCAAGAGGCTTACGCTTGTCTCTCCCTCT 1167
QY 394 GluLeuPheIleProValGluAspAspValMetGluArgGluArgLeuIleGluSerVal 413
DB 1168 GCTCTCTTACCCCGCGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1227
QY 414 ProAspSerValThrProLeuIleIleTyrGluGluGluThrAspIleThrIleAsnIle 433
DB 1228 CCCAAGATGTGCGACCCCTTGTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1287
QY 434 HisAspIlePheHisValPheProGluSerHisGluGluGluGluPheIlePhe 452
DB 1288 CACGACATCTTCCACCGCTTCTCAGGCTGAGGCGAGCGAGAGAGAGAGAGAGAG 1347
QY 453 AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu 472
DB 1348 GCCAAGCATATGACAGACGCTTGTGACCTGTACAGAGAGAGAGAGAGAGAGAGAGAG 1407
QY 473 SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle 492
DB 1408 AAGGACTATGCTGAGCGAGAAACCCCTCAGCCCTACAGAGAGAGAGAGAGAGAG 1467
QY 493 LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGluArgHisGlySerAsn 512
DB 1468 AAGGAGAGGCTGCGCTGACAGTGGAGAGTGTGTGTGAGAGAGAGAGAGAGAGAG 1527
QY 513 IleGluValAspGluValArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu 532
DB 1528 ATCTGGGCAACAG 1587
QY 533 GluHisHisLeuTyrValIleSerTyrValAsnProGlyGluValThrArgLeuThrAsp 552
DB 1588 GAACATACCTATGTGCTGACAGTACAGTACAGCAGGAGAGAGAGAGAGAGAGAGAG 1647
QY 553 ArgLysTyrSerHisSerCysIleSerGlnHisCysAspPheIleSerLysTyr 572
DB 1648 CTCTGCTTCTCCACAGCTGTCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1707
QY 573 SerAsnGluLysAsnProHisCysValSerLeuTyrLysLeuSerProGluAspAsp 592
DB 1708 AGCAGTGTGAGACAGCAGCAGCTGTGATCATGTATACAGAGAGAGAGAGAGAGAGAG 1767
QY 593 ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro 612

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Db 1768 CCACTGACAGAACACCGCTTCTGGGCCAGCATGATGAGAGCCCAATTGCCCCCA 1827
Qy 613 AspyrThrProProGluIlePheSerPheGluSerThrThrGlyPheThrLeuTyrGly 632
Db 1828 GACTATGTGCCCCCTGAGATCTTCCACTTCCACACCCGTCGACAGCTGCTTACGGC 1887
Qy 633 MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle 652
Db 1888 ATGATCTACAGACACACACCTGCAACCTGGGAGAGACCCACCTGCTCTTTGTC 1947
Qy 653 TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg 672
Db 1948 TATGGGGGCCACAGAGCTGAGTGAACACCTTTTAAGGCGATCAATGACTCTCGC 2007
Qy 673 LeuAsnThrLeuAlaSerLeuGlyTyrValValValValIleAspAsnArgGlySerCys 692
Db 2008 CTAAATACACTGCGATCTTGGGCTATGCTGTGTGTGATCGATGGTCTGGGCTCTGT 2067
Qy 693 HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp 712
Db 2068 CAGCGGGGCTGCACTTGCAGGGGGCCGAAATCAATGCGCCAGTGGAGATTGAG 2127
Qy 713 AspGlnValGluLeuGlnTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg 732
Db 2128 GACCAGGTGAAGAGCTTGCAGTACGTGAGAGTATGCTTCAATGACTTGCACCGCA 2187
Qy 733 ValGlyIleHisGlyTyrSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg 752
Db 2188 GTGGCCATCATGGCTGTGCTTACGGGGCTTCTCTCACTCATGAGGGCTCATCCACAG 2247
Qy 753 SerAspIlePheArgValAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 772
Db 2248 CCACAGAGTGTCAAGAGTACGATGGCGGGCTCTCTCACTGATGATGAGGCTATGAC 2307
Qy 773 ThrGlyTyrThrGlnArgTyrMetGlnLysProAspGlnAsnGlnGlnGlyTyrTyrLeu 792
Db 2308 ACAGGGTACAGGAGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2367
Qy 793 GlySerValAlaMetGlnAlaGlyLysPheProSerGluProAsnArgLeuLeuLeu 812
Db 2368 GGGTGTGTACCGCTGCATGTGAGAGAGCTGCCAATGAGCTAAGCCCTGATTATCTC 2427
Qy 813 HisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu 832
Db 2428 CAGGGCTTCTGAGAGAGAGCTTCACTTCTCCACAAATTTCTGTCCTCCACCTG 2487
Qy 833 ValArgAlaGlyLysProTyrAspPheGlnIleTyrProGlnGlnArgHisSerIleArg 852
Db 2488 ATCCGAGCAGGAAGCCATATCAGACTTACCCAAACGAGACATAGCATCCGC 2547
Qy 853 ValProGluSerGlyGlnHisTyrGlyLeuHisLeuLeuHisTyrGlyLeuGlnGlnLeu 872
Db 2548 TGGCGGAGTCCGGAGAGCATTTAGAGGTGACGCTGTGCACCTTCTGACAGAACACTG 2607

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RESULT 22
ABK83339
ID ABK83339 standard; cDNA; 4180 BP.

AC ABK83339;

DT 12-AUG-2002 (first entry)

DE cDNA encoding human DPRP-2 splice variant #7;

XX Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;
KM DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KM diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
KM heart failure; hypertension; urinary retention; osteoporosis; cancer;
KM ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KM dyslexia; reproductive disorder; inflammatory disorder;
KM metabolic disorder; gene; ss.

OS Homo sapiens.

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XX XX
PN MO200231134-A2.
PD 18-APR-2002.
XX 12-OCT-2001: 2001MO-US31874.
XX 12-OCT-2000: 2000US-240117P.
XX (FERR ) FERRING BV.
XX Q1 S, Akinsanya KO, Riviere PJ, Junten J;
PI WPI: 2002-444178/47.
XX P-PSDB: ABG61608.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
PS Disclosure: Page 97-98: 113pp: English.
XX
XX The present invention relates to the isolation of novel human serine
XX proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
XX proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
XX and nucleic acids encoding them are useful for treating infections
XX such as fungal, bacterial, protozoan and viral infections, particularly
XX infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
XX pain, diabetes, precocious puberty, infertility, obesity, anorexia,
XX bllimia, Parkinson's disease, acute heart failure, hypotension,
XX hypertension, urinary retention, osteoporosis, angina pectoris,
XX stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
XX psychotic and neurological disorders (e.g. anxiety, dementia, or
XX schizophrenia), and dyslexias. These may also be used in discovering
XX therapeutic agents for the treatment of reproductive, inflammatory and
XX metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
XX
SQ Sequence 4180 BP; 898 A; 1312 C; 1178 G; 792 T; 0 other:

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Alignment Scores:

Pred. No.:	9.67e-278	Length:	4180
Score:	2820.50	Matches:	510
Percent Similarity:	76.43%	Conservative:	132
Best Local Similarity:	60.71%	Mismatches:	183
Query Match:	60.01%	Indels:	15
DB:	24	Gaps:	3

US-10-070-464-1 (1-882) x ABK83339 (1-4180)

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Qy 35 PheTyrValGluArgTyrSerThrProSerGlnLeuLysLeuLeuAlaAspThrArgLys 54
Db 436 TTCCAGGTGACGAGAGCATCTGTGGAGCGGCTCCGGAGCATATCCACGGACGGCAG 495
Qy 55 TyrHisGlyTyrMetAlaLysAlaProHisAspPheMetPheValLysArgAsnArg 74
Db 496 TACTCGGGCCCTCATTTGCAACAGGGCCGCCACACACTTCCAGTTGGTGGAGAGAGCAT 555
Qy 75 ProAspGlyProHisSerAspArgIleTyrTyrTyrLeuAlaMetSerGlyGlnAsnArgGln 94
Db 556 GAGTCTGGGGCCCTCCACCTCCCTACTACTGCGAATGCGCATATGCGAGCCGAGAG 615
Qy 95 AsnThrLeuPheTyrSerGluIleProLysThrIleAsnArgAlaAlaValLeuMetLeu 114
Db 616 AACCTCCTCTTACTTGTGAGATTCCCAAGAGAGTCCGGAAGAGCTTGTGCTCTCG 675
Qy 115 SerThrLysProLeuAsnAspLeuPheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
Db 676 TCTCGAAGCAGANTGCTGATTCATTCACAGGCCACGCCACCATGAGGCTACTCTCGG 735
Qy 135 GluGlnGluLeuLeuArgGluArgLysArgIleGlyThrValGlyIleAlaSerTyrAsp 154
Db 736 GAGAGAGAGCTGTGAGAGAGCGAAGCCCTGGGGCTTTCGCGACACCTCTTACGAC 795

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OY	155	TYRHISGLNGLYSERYTHRPHLEUPHGLNALAGLYSERGLYLLETHRHISVALYS	174
DB	756	TTCCACACCGAGACTGGCTTCCTTCCTCCAGGACGACAGACGCTTCCTCAGCGCGC	855
OY	175	ASPGLYGLYPROGLINGLYPHETHRGLNGLNPROLEUAIRPROASNLEUVALGLTHRHSR	194
DB	856	GACGGCGGACGAAGACGGCTTCATGCTGTCCCTATGAACCCCTGGAAATCAAGACCGAG	915
OY	135	CYSPROASNILEARGMETLEASPTRYLSLEUCYSPROALASPPROASPTIRLEALPHE	214
DB	916	TGCTCAGGGCCCGGATGGAGCCCAAAATCTGCCCTGGCCGACCTGCTTCCTTCCTTC	975
OY	215	ILEHISSEASASPILETETTRIPLESERASNILEVALTHIRGLINGLUNARGHLEUTHR	234
DB	976	ATCATATACACGACGACCTGTGGTGGCCACATCGAACACAGGAGAGCGGGCTGACC	1035
OY	235	TYRVALHISASNGLULEUALASNMETGLULASPALARGSERALAGLYVALALATHR	254
DB	1036	TTCTCCGCCCAAGGTTTATCCATATGCTCCGAGATGCCCAAGCTGCGGGGTGGCCACC	1095
OY	255	PHENVALLAUNGINGLUNGLPHEASPARGLYTSERGLTYRTRTPRCYSPROLYSVALIU	274
DB	1096	TTTCGTCATACACGAGAGAGTTCCAGCCGTTACTGGTACTGCTGTGCCCCACACGCTCC	1155
OY	275	THRTHRPROSERGLYGLY---LYSILELEUAARGILELEUTYRGLULNASAPOLUSER	293
DB	1156	TGGGAGAGGTTCCAGAGGGCCCTCAAGACGCTCGAATCCTGTAGAGAGTGCATGATGCC	1215
OY	294	GLUVALIGLUILEHISVALTHRSEPROMETLEUNGITHIRARGARALASPERPHE	313
DB	1216	GAGGTGGAGGTCATTCACGTCCTCCCTCCGCGCTAGAAAGAAAGACGGAGCTCGAT	1275
OY	314	ARGTYRPROLYSTHRGLYTHRILALASNPROLYSVALTHIRPHELYSMESERGLUIMET	333
DB	1276	CGGTACCCCGAGACAGGACAGCAAGATCCACAGATTGGCTTGAACCTGGCTGATGTTCCAG	1335
OY	334	ILEASPALAIGLUGLYARGILEILEASPVALLASPVLYSGLULEUULEGNIPTROPHCLU	353
DB	1336	ACTGCACCCGAGGCGCAAGATCGTCTGCACCCAGAGACAGAGACTGGTGCAGCCCTTCAGC	1395
OY	354	ILELEUPHEGLUGLYVALIGLYTYRTHIRLEALARGALAGLYTRPTHRPROGLUPLYSTYR	373
DB	1396	TGCGCTGTTCCCGAAGGTGGAGATCATGCCAGGGCCGGGTGGACCCGGGATGCAAAATAC	1455
OY	374	ALATRPSEIRILELEUAUSPARYSERGLNTHIRARGLEUNGILVEALILEUULESERPRO	393
DB	1456	GCTCTGGCCCATGTCCTGGACCGGCCCCACAGATGCTCCACATCGTCTCCTCCGCCCG	1515
OY	394	GLIUEUPHEIIEPROVALIGLUNASPAAPVALMEGLIARGGLNARGLEULELSERVAL	413
DB	1516	GCCCTGTTCACTCCGACACAGAAATGAGAGACACGGCTTAGCCTTCGCCAGACTTC	1575
OY	414	PROASPERVALTHIRPROLEUULEILETYRGLUGLITHIRASPILETIRPLEASNILE	433
DB	1576	CCGAGAGATGTCGACCGGTATGTCGTGTACGAGAGCTCACCAACGTCGTGATCATGTT	1635
OY	434	HISASPILEPHEHISVALPHEPROGLINSEHIS---GLINGLUGLIEGLUPHEILEPHE	452
DB	1636	CATGACATCTTCATCCCTCCCTCCCATCAGAGGAGAGGACACTCTGCTCTCTCCGC	1695
OY	453	ALASERGLUCYLSYSTRHGLYPHEATGHSILEUTYRLYSILETHSERILEUENUGSLU	472
DB	1696	GCCATATGATACAGACCGGCTTCTGCATTTTACAAAGTACACCGCGTTTAAAAATCC	1755
OY	473	SERYLSYRILYSARGSERSERGLYGLYLEUPROALAPROSERASPHELYSCYSPROILE	492
DB	1756	CAGGCGTACGATGGATGTAGACCTTCAGCCCCGGGAGAGATGAATTAAGTCCCATTT	1815
OY	493	LYSLGLUGLUILEALILETHRSEIRGLYGLUTRPGULVALLEUGLYARGHISGLYSERASN	512
DB	1816	AAGGAGAGATTTGCTTCGACACCGGTGAATGGAGAGTTTGGCAGAGCAGCGCTCC---	1872

QY	513	ILGGINValAspGluValAlaArgLeuValTyrPhgGluTyrThrLysAspSerProLeu	532
Db	1873	-----AAAGGACCAAGAGACGGCGGTG	1896
QY	533	GIuHisHisLeuTyrValAlaSerTyrValAsnProGluValThrArgLeuThrAsp	552
Db	1897	GAGCAACCACTCTACGGTGGTACGTATGAGCGCGCGGAGAGATGGTACCGACAG	1956
QY	553	ArgGlyTyrSerHisSerCysLysIleSerGlnHisCysAspPheMetIleSerLysTyr	572
Db	1957	CCCGGCTTCTCCATACCTCTCTCCATGAGCAAACTTGCAATGTGTGTCAGCCATAC	2016
QY	573	SerAsnGlnLysAsnProHisCysValSerLeuTyrLysLeuSerSerProGluLysAsp	592
Db	2017	AGCAAGCGTACAGACGGCGCGCTGGTGCACGCTTACAACTGAGCGCGCCGAGCAGAC	2076
QY	593	ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	2077	CCCGCGCAAGCAAGCGCCGCTCTGGCGGTAGCATGATGAGGACAGCATGCCCCCG	2136
QY	613	AspTyrThrProProGluIlePheSerPheGluSerThrThnGlyPheThrLeuTyrGly	632
Db	2137	GATTATGTCTCTCCAGAGATCTTCATTTCCACACCGCGTGGATGTGCGGTCTACGGC	2196
QY	633	MetLeuTyrLysProHisAspLeuGlnProGlyLysLysTyrProThrValLeuPheIle	652
Db	2197	ATGATCTACAGCCCGCCAGCGCTTGCGACCGAGGAAACACCCCGCTCTTTGTGA	2256
QY	653	TyrGlyLysProGlnValGlnLeuValAsnAsnArgPheLysGlyValLysTyrPheArg	672
Db	2257	TATGAGGCGCCCGAGGTCAGCTGGTGTAAATCTCTTAAAGGATCAAGACTTGGCG	2316
QY	673	LeuAsnThrLeuAlaSerLeuGlyTyrValValValIleAspAsnArgGlySerCys	692
Db	2317	CTCAACACACTGGCGTCCGTGGCTACCGCGTGTGATTAGCGCAGGGGCTCTGT	2376
QY	693	HisArgGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyGlnIleGluIleAsp	712
Db	2377	CAGGAGGCGTTCGGTTGCGAAGGGCGCTGGAATAAACCAATGGCGAGGTGAGTACAG	2436
QY	713	AspGlnValGlnGlyLeuGlnIleTyrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732
Db	2437	GACCAGGTGAGGGCGCTGCAGATTCGTGCCGAGAACTATGCTTCATCGACTGACGCGA	2496
QY	733	ValGlyIleHisGlyTyrPserTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2497	GTTGGCATTCGATGGCTGTCTACGGGGGCTTCCTCCCTCATGGGGCTATCCACACAG	2556
QY	753	SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp	772
Db	2557	CCCCAGGCTTCAAGGGTGGCCATTCGGGGGTGCCCGGTACCGGTGGATGGCCCTACAC	2616
QY	773	ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnIleTyrThrLeu	792
Db	2617	ACAGGTTACACTGAGCGCTCATGTGACGTCCTCGAACAACACACACAGCGCTATGAGCG	2676
QY	793	GlySerValAlaMetGlnAlaGlyLysPheProSerGlnProAsnArgLeuLeuLeu	812
Db	2677	GTTTCCGGTCCCTGCACGCTGGGAAGACTGCCAATGAGCCCAACCGCTGTGTTCTCTC	2736
QY	813	HisGlyPheLeuAspArgGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu	832
Db	2737	CACGGCTTCCGGAGCAAAACGTGCACTTTTCCACACAACTCTCTGTCGCCAATG	2796
QY	833	ValAlaGlnGlyLysProTyrAspLeuGlnIleTyrProGlnGluArgHisSerIleArg	852
Db	2797	ATCCGAGCAGGAAACCTTACACAGCTCCAGATCTACCCCAAGAGACACAGTATTGCG	2856
QY	853	ValProGluSerGlyGluHisTyrGluHisLeuLeuHisTyrLeuGlnGluAsnLeu	872
Db	2857	TGCCCCAGATCGGGCGAGCACTATGAAGTACAGTTGCTGCTCACTTCTTACAGGAATACCTC	2916
RESULT 23			

RESULT 23

Db	1576	CCAGGAATGTCACGCGCTATGTGGTGTACAGAGAGTCCACCAAGCTCTGATCAATGTT	1635
QY	434	HISAPLIEPHEHISVALPHEPROGLINSEHIS---GLUGLUGLIEUPLHE	452
Db	1636	CATGACATCTTCTTATGCCCTTCCCAATCAGAGAGAGAGAGAGCTGTGCTTCTCCG	1695
QY	453	ALASERGLUCYSLYSTHNGIPHEATGNHISLEUTYLSILETHSERILEUENYSGLU	472
Db	1696	GCCATGATGATCCAGACCGGGCTTCTGCAATTGTTACAAAGTCAACCGCTTTAAATCC	1755
QY	473	SERYLYSTLYSARGSERISERYGLYLEUPROALAPROSERASPHELYSCYSPROLE	492
Db	1756	CAGGCGATCGATGGATGGATGACCCCTTGACGCCCGGGGAAGATCAATTAAAGGCCCAT	1815
QY	493	LYSGUGLUILEALILETHSERGLYGLUTRPGLIVALLEUGLYARGHISGLYSERAN	512
Db	1816	AAGGAGAGATGCTCTGACCAACCGGAGATGGAGAGTTTGGCAGGACGCGCTC---	1872
QY	513	ILEGLVALASPLUVALARGATGLEUVALTYRPHGLUGLYTHRLYSASPERPROLEU	532
Db	1873	-----AAGGACACAGAGACACGCGCGCTG	1896
QY	533	GLINHISLEUTYRVALVASETYRVALASPROGLIVALLTHARGLEUHRASP	552
Db	1897	GAGCACCACTCTACGTGGTACAGTGAAGCGCGCGGAGAGATCTAGCGCTCAACAG	1956
QY	553	ARGGLYTRSERHISSERCYSILESERGLINHISCYSPASPHEHILLESELYSTYR	572
Db	1957	CCCGGCTTCTCCATACTGCTCCATGAGCAGAACTTGACATGTGCTGACGACATAC	2016
QY	573	SERASNGLYSANPROHISCYSPVALSERLEUTYRLYLEUSERSERPROGLIUSPASP	592
Db	2017	AGCGACGTGACACGCGCGCTGCGTGCACAGTTCACCTGACGCGCGCGACGACAC	2076
QY	593	PROTHRYSLYSTHRLYSGUPHETPALATHILELEASPERALACLYPROLEUPRO	612
Db	2077	CCCGTACGACAGACGCCCGCTTCTGGCGTAGCATGATGAGAGGACGACGTCGCCCCG	2136
QY	613	ASPLYRTHRPROPROGLIUIEPHESERPHIEGLUSERTHTHGLYPHERHLEUTRYGL	632
Db	2137	GATATATGTTCTCCAGAGATCTTCATTTCCACACCGCGCTGGAGTGGCGCTACAGCG	2196
QY	633	METLEUTYRLESPROHISASPLIEUENPROGLYLSGLYSTYRPROTHYVALLEUHELLE	652
Db	2197	ATGATCTACAGGCCCAACGCGCTTGACACCGAGAAACACCCACGCTCTCTTTGTA	2256
QY	653	TYRGLYGLYPROGLINVALINLEUVALASDASDARGPHELYSGLYVALYLYSTYRPHEAR	672
Db	2257	TATGGAGGCCCCCAGGTGACAGCTGTGTAAATACCTCTTAAAGGCTACAGTACTTGGCG	2316
QY	673	LEUASDTHRLLEUASERLEUGLYTYRVALVALVAILLEASPSANRGLYSERCYS	692
Db	2317	CTCAACACACTGGCGCTCCCTGGGCTACGCCGTGTGTGATTGACGCGAGGGGCTCTGT	2376
QY	693	HISARGLYLEUENYSPHEGLUGLYALAPHELYSTYRLYSMETGLYGLINLEGLIUEAS	712
Db	2377	CAGCGAGGGCTTCGGTTCCGAAGGGGCGCCCTGAANAACCAATGGCGCAGGTGAGATCGAG	2436
QY	713	ASPLINVALIGLUGLYLEUGLINTYRLEUALASERATRYASPHEHLEASPLEUASPAR	732
Db	2437	GACCAAGGTGGAGGGCTCGACAGTTCTGTGGCGGAAAGATATGAGCTTATCCATCCGTGAGCGGA	2496
QY	733	VALGLYLEHISGLYTRPSETRYGLYGLYTYRLEUSERLEUENVALLEUENGLINRG	752
Db	2497	GTTGCGACATCATGGCTGCTCTTACGGGGGCTTCTCTCGCTATGGGGCTAATCCACAAG	2556
QY	753	SERASPLIEPHEARGVALAILEALAGLYALAPROVALTHNLEUTRPLIEPHEURYASP	772
Db	2557	CCCCAGGTGTCAAGGTGGCCATCGGGGGGCGCCCGGTACACGTCTGATGAGCTTATGAGCG	2616
QY	773	THHGLYTRHNGLYARGYRMETGLYHISPROASGLINASGLUGLNGLYTYRTRYLEU	792
Db	2617	ACAGGTTACATGAGCCCTACATGAGAGTCTCCGAAACACACAGACGACGCGATATGAGCG	2676

QY	793	GlyserValAlaMetGlnAlaGluValysPheProSerGlnProAsnArgLeuLeuLeu	812
Db	2677	GGTTCGCGGGCCCTGGCAACGTGGAGAAAGCTGCCAAAGAACCCCAACCGCTGTATCTCC	2736
QY	813	HisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleuLeuSerPheLeu	832
Db	2737	CACGAGTCTCTGGACGAAACGTGCACCTTTTCCACACAAACTCTCTGCCAACTG	2796
QY	833	ValArgAlaGluysProTyrAspLeuGlnIleTyrProGlnGlnArgHisSerIleArg	852
Db	2797	ATCCGACGAGGAAACCTTACACAGCTCCGAACTCTACCCCAACGAAAGACACAGTATTGCG	2856
QY	853	ValProGluSerGlyGlnHisTyrGlnIleuHisPheLeuHisTyrLeuGlnIleuAsnLeu	872
Db	2857	TGCCCGAGTGGCGGCGAGCACTATGAAGTCAGCTTCTGCTCAAGAAATACCTC	2916
RESULT 24			
ID	AAD38311	standard; cDNA; 2751 BP.	
XX	AAD38311:		
AC	AAD38311:		
DT	23-SEP-2002	(first entry)	
XX			
DE	Murine dipeptidyl peptidase 9 (DPP9) cDNA.		
XX			
KW	Murine: dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection;		
KW	human: immuno deficiency virus; graft rejection; cytostatic; autoimmunity;		
KW	type II diabetes; antidiabetic; antiinflammatory; immunosuppressive;		
KW	antiviral; enzyme; gene; ss.		
OS	Mus sp.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	2..2545	
FT		/*tag= a	
FT		/product= "Murine DPP9 protein"	
FT		/note= "CDS does not include start codon"	
FT		/partial	
XX			
PN	W0200234900-AL.		
XX			
PD	02-MAY-2002.		
XX			
PF	29-OCT-2001; 2001WO-AU01388.		
XX			
PR	27-OCT-2000; 2000AU-0001078.		
XX			
PA	(UNSY) UNIV SYDNEY.		
PI	Abbott CA, Gorrell MD;		
XX			
DR	WPI: 2002-454646/48.		
XX	P-PSDB: AAE23875.		
XX			
PT	New dipeptidyl peptidase (DPP) peptidases, useful for screening		
PT	inhibitors of DPP catalytic activity, which may be employed to treat		
PT	e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft		
PT	rejection and HIV infection -		
XX			
PS	Disclosure; Fig 9; 91pp; English.		
XX			
CC	The present invention relates to dipeptidyl peptidase (DPP) proteins and		
CC	polynucleotides encoding such proteins. The DPP peptidases are useful		
CC	for screening inhibitors of DPP catalytic activity. The inhibitors are useful		
CC	for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft		
CC	rejection and HIV (human immuno deficiency virus) infection. The present		
CC	sequence is an alternative version of murine DPP9 cDNA.		
CC	Note: This sequence is stated to be the same as that shown as		
CC	SEQ ID NO: 3 in the sequence listing of the specification. However these		
XX	sequences differ.		

[illegible]

Db 2009 CTAATACACCTGCATCCCTGGGCTATGCTGTCGCTGGTATCGAATGCTCGGGCTCCCTGT 206

Qy 693 HisAcGlyLeuLysPheGluGlyAlaPheLysTyrLysMetGlyClnIleGluLeuAsp 712
||||||| ||||||||| ||| ::||| |||||:::|||||:::

Db	2069	CAGGGGGCCCTGCACCTTCGAGGGGGCCCTGAAATAATCAATATGGCCAGGTGGAGATTGAG	212	8
QY	713	AspGlnValGluGlyLeuGlnIYrLeuAlaSerArgTyrAspPheIleAspLeuAspArg	732	8
Db	2129	GACCAAGGTGGAAAGGCTTCGAGTCCGGGGGAGAAAGTATAGGCTTATTTAGTACTGAGGCCA	2188	8
QY	733	ValGlyIleHisGlyTrpSerTyrGlyGlyTyrLeuSerLeuMetAlaLeuMetGlnArg	752	8
Db	2189	GTCGGCATCCATGGCTGCTGCTCTAGGGGGGCTTCCTCTACATGATGGGCTCATCCACAG	2248	8
QY	753	SerAspIlePheArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyrAsp	772	8
Db	2249	CCACAAGTCTTCAAGGTAGGCATTGGGGGGCTCTGCTACGTGTGGATGGCCATTATGAC	2308	8
QY	773	ThrGlyTyrThrGluArgTyrMetGlyHisProAspGlnAsnGluGlnIYrTyrLeu	792	8
Db	2309	ACAGGGTACACGAGACCATATCATGTGATGTCCTCCGAAATAATACCAGCAGCATATGAGCA	2368	8
QY	793	GlySerValAlaMetGlnAlaGlyLeuGlyLeuPheProSerGluProAsnArgLeuLeuLeu	812	8
Db	2369	GGGTCTGAGCCCTGCATGTGGGAAAGCTCCCAATAGACCTAACCGGCTGTATCTTC	2428	8
QY	813	HisGlyPheLeuAspGluAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLeu	832	8
Db	2429	CACGGCTTCGAGCAGAAAGCTTCACCTTTCACACAAATTTCCGTGTGCCAGCTG	2488	8
QY	833	ValArgAlaGlyLysProTyrAspLeuGlnIle-----	843	8
Db	2489	ATCCGAGCAGGAAAGCATATACAGTTCACAGT-TGCATCATGACACAAACCTCAGTACT	2547	8
QY	843	-----	843	8
Db	2548	ACCCTCAGTAAAGCCCACTTTTGATGAACCCACTTGGCTACAGGATGGAGTGGCCC	2607	8
QY	843	-----	843	8
Db	2608	CCAATGATTAGAGCCCAAGACGAGTGGCTGAGGGAGAGACATTTAAGSTCCAGAGAC	2667	8
QY	844	-----TyrProGlnGluArgHisSerIleArgValProGluSerGlyLeuHisTyrGlu	861	8
Db	2668	TGAATCTCTACCCAAAGAGAGACATATAGCATCCGTGCCGCGAGTCCGAGAGCATTAACGAG	2727	8
QY	862	LeuHisLeuLeuHisTyrLeuGln	869	8
Db	2728	GTAGCGCTGCTGCACCTTCTGCGG	2751	8
RESULT 25				
ABK83337				
ID	ABK83337	standard; cdna; 4076 bp.		
AC	ABK83337;			
XX				
DT	12-AUG-2002	(first entry)		
XX				
DE		cdna encoding human DPRP-2 splice variant #5.		
XX				
KW		Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;		
KW		DPRIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;		
KW		diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;		
KW		heart failure; hypertension; urinary retention; osteoporosis; cancer;		
KW		ulcer; allergy; cancer; psychotic disorder; neurological disorder;		
KW		dyskinesia; reproductive disorder; inflammatory disorder;		
KW		metabolic disorder; gene; ss.		
XX				
OS	Homo sapiens.			
XX				
PN	WO200231134-A2.			
XX				
PD	18-APR-2002.			
XX				
PF	12-OCT-2001; 2001MO-US31874.			
XX				
PR	12-OCT-2000; 2000US-240117P.			

[illegible]

Oy	195	CysProAsnIleAmeTAspProLysIeuCysProAlaAspProAspTrpIleAlaPhe	214
Db	916	TGCTCAGAGCCCGGATGGACCCCAAAATTCGCCCTCGCCAGCCCTTCCTTCCTTC	975
Oy	215	IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgIuGluIuArgArgLeuThr	234
Db	976	ATCAATTAACAGCGACCGTCGTGGTGGCCAACTCGACAGACGCGAGAGCGGGCGGTGAC	1035
Oy	235	TyrValHisAsnGluLeuAlaAsnMetGluIuAspAlaArgSerAlaGlyAlaIaThr	254
Db	1036	TTTCGCCACCAAGATTATTCATGTCTCGGATGACCCCAAGTCGCGGGTGTGGCCAC	1095
Oy	255	PheValLeuGluGluIuPheAspArgTyrSerGlyTyrTrpTrpCysProLysIaGlu	274
Db	1096	TTTCCTCATACAGGAAGATTCCAGCCCTTCACCTGGTACTGTGGTGGCCACAGCTTC	1155
Oy	275	ThrThrProSerGlyGly--LysIleLeuArgIleLeuTyrGluIuAsnAspIuSer	293
Db	1156	TGGGAAGTTTACAGAGGCCCTCAAGACGCTCGCGAATCCTGTATAGAGAGTCGATGATCC	1215
Oy	294	GluValGluIleIleHisValThrSerPromLeuGluThrArgAlaAlaSerPhe	313
Db	1216	GAGGTGAGGTCAATCAGCTCCCTCTCTCGCGCTAGAAAGAAAGACGCACTCGAT	1275
Oy	314	ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluIleMet	333
Db	1276	CGGTACCCCAAGACAGCACAGCAAGATCCCAAGATTGCTTGAACCTGGCTGATTCAG	1335
Oy	334	IleAspIaGluGluArgIleIleAspValIleAspLysGluIleIleGlnProPheIu	353
Db	1336	ACTGACAGCCAGGCAAGTCGCTCGCCACCCAGGAAAGACCTGTGTACAGCTTCACGC	1395
Oy	354	IleLeuPheGluGluValGluTyrIleAlaArgAlaGlyTrpThrProGluGlyLysTyr	373
Db	1396	TGCGTGTTCGCAAGGAGGAGTCAATCGCCAGGCGCGGTGGACCCGGGATGGCAAAATAC	1455
Oy	374	AlaTrpSerIleLeuLeuAsnParGserGlnThrArgLeuGlnIleValIleuIleSerPro	393
Db	1456	GCGTGGGCGCATGTTCTCGACCGCGCCAGCAAGTCGCTCACCTGCTCTCCGCCCCG	1515
Oy	394	GluLeuPheIleProValGluAspAspValMetGluArgIuArgIleuIleuSerVal	413
Db	1516	GCCCTGTATCCCGAGACACAGAAATGAGAGACAGCGGCTGACCTGCCAGAGCTTC	1575
Oy	414	ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle	433
Db	1576	CCCGAATTCACCGCGCTGTGGTGTACGAGAGAGTCACCAACGTGTGATCAATGTT	1635
Oy	434	HisAspIlePheHisValPheProGlnSerHis--GluGluGlnIleGlnPheIlePhe	452
Db	1636	CATACATCTTCTATCCCTTCCCCCAATGAGAGGAGAGAGACACTGCTTCTTCGCC	1695
Oy	453	AlaSerGluCysLysThrGlyPheArgHisLeuTyrLysIleThrSerIleLeuIuGlu	472
Db	1696	GCCAAATGAAGCAAGACCGGCTCTGCCATTTGTACAAAGTACCGCGGTTTAAATTC	1755
Oy	473	SerLysTyrLysArgSerSerGlyGlyLeuProAlaProSerAspPheLysCysProIle	492
Db	1756	CAGGGCTACGATTTGGATGTGCGCTTCACCGCGGGAAGATTAATTAAGTCCCAATT	1815
Oy	493	LysGluGluIleAlaIleThrSerGlyGluTrpGluValLeuGluYArgHisGlySerAsn	512
Db	1816	AAGGAAGAAATGCTGTGACACCGGTGAATGGAGAGTTTGGCAGGCAAGCGCTCCAG	1875
Oy	513	IleGlnValAspGluValaArgArgLeuValTyrPheGluGlyThrLysAspSerProLeu	532
Db	1876	ATCTGGGTCAATGAGGAGCAACAGCTGTGTGTACTTCCAGGCAACCAAGACACGCCCTG	1935
Oy	533	GluHisHisLeuTyrValIleSerTyrValAsnProGluGluValaThrArgLeuThrAsp	552
Db	1936	GAGACCAACCTCTACGTGGTCACTTGAAGCGCGCGGCGGAATGTGATGCGCTTCAACG	1995

Oy	553	ArgelgyrSerHisSerCysCysIleSerGlnHisCysAspPheIleSerIlysr	572
Db	1996	CCCCGCTTCTCCCACTACTCTCCATGAGCAAACTTCGATGCTGCAGCCACTAC	2055
Oy	573	SerAsnGlnLysAsnProHisCysValSerLeuTyLysLeuSerSerProGlnAsp	592
Db	2056	AGCAAGCGAGACACGGCCGCGTGCAGCTTACACAGTACAGGGGCCCGACAGACAC	2115
Oy	593	ProThrCysLysThrLysGluPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	2116	CCCCGCAACAAGCAGCCCGCTCTCGGGCTAGCATGATGATGAGGACGACGCGCCCGG	2175
Oy	613	AspTyThrProProGluIlePheSerPheGluSerThrThGlyPheThrLeuTyGly	632
Db	2176	GATTATGTCTCCAGAGATCTTCATATTCACACCGCGTGGATGTGGCTCTACGGC	2235
Oy	633	MetLeuTyLysProHisAspLeuGlnProGlyLysLysTyProThrValLeuPheIle	652
Db	2236	ATGATCTTACAGCCCCACGGCTTCGACGCCGAGAGACACCCACCGCTCTTGTGA	2299
Oy	653	TyrGlyGlyProGlnValGlnLeuValAsnAsnArgPheIleGlyValLysTyPheArg	672
Db	2296	TATGAGAGCCCCCAGGTCAGCTGTGTGAATAACTCTTCAAAAGCATCAAGTACTGGG	2355
Oy	673	LeuAsnThrLeuAlaSerLeuGlyTyTyValValValIleAspAsnArgLysCys	692
Db	2356	CTCAACACACTGGCTCTCCGGCTACGCCGCTGGTGTATTTACAGCGAGGGGCTTCGT	2415
Oy	693	HisArgGlyLeuLysPheGluGlyAlaPheLysTyLysMetGlyGlnIleGluLeasp	712
Db	2416	CAGCGAGGGCTTCGGTTCGAAAGGGCCCTGAAAAACCAATGGCCAGGTGAGATCGAG	2475
Oy	713	AspGlnValGlnGlyLeuGlnTyLysAlaSerArgTyAspPheIleAspLeuAspArg	732
Db	2476	GACCAAGGAGGAGGCGCTGACGATTCGTGGCCGAGAGATGATGGCTTCACCTGAGCGGA	2535
Oy	733	ValGlyIleHisGlyTrpSerTyGlyGlyTyLysLeuSerLeuMetAlaLeuMetGlnArg	752
Db	2536	GTTCGCATTCCTATGGCTGTGCTACAGGGGCGCTTCCTCGCTCATGGCGTAATCCACAAG	2595
Oy	753	SerAspIlePhe-ArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTyAs	772
Db	2596	CCCCAGGCTTCAAGG-----	2611
Oy	772	PThrGlyTyThrGlnArgTyTrpMetGlyHisProAspGlnAsnGluGlnGlyTyTrpLe	792
Db	2611	-----	2611
Oy	792	uGlySerValAlaMetGlnAlaGluLysPheProSerGluProAsnArgLeuLeuLeuLe	812
Db	2612	-----CCCAACCGCTTCTATCTCT	2631
Oy	812	uHisGlyPheLeuAspGlnAsnValHisPheAlaHisThrSerIleLeuLeuSerPheLe	832
Db	2632	CCAGGCTTCTTGACCAAAAAGTGCACCTTTTCCACACAAAATCTTGTTCCCAACT	2691
Oy	832	uValArgAlaGlyLysProTyArgAspLeuGlnIleTyTrpProGlnGluArgHisSerIleAr	852
Db	2692	GATCGAGACAGGAACCTTACACAGCTCCAGATCTACCCCAACGAGACACAGATTTGG	2751
Oy	852	gValProGluSerGlyLysIleTyTrpGluLeuHisIleLeuLeuHisTyTrpGluGlnGluAsnLe	872
Db	2752	CTGGCCCGAGTGGCGGCGAGCACTATGAAAGTCAACGTTGCTGCACCTTTCTACAGAAATACCT	2811
Oy	872	u	872
Db	2812	C	2812
RESULT 26			
ABK83336			
ID	ABK83336 standard; cDNA; 4159 BP.		
AC	ABK83336;		

XX 12-AUG-2002 (first entry)
 DE CDNA encoding human DPRP-2 splice variant #4.
 XX
 KW Human: serine protease: dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder; gene; ss.
 XX
 XX Homo sapiens.
 OS
 PN MO200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001MO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX
 PA (FERR) FERRING BV.
 XX
 PI Q1 S, Akinsanya KO, Riviere PJ, Junten J;
 XX
 DR WPI: 2002-444178/47.
 XX
 DR P-PSDB; ABG61605.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 XX
 XX Disclosure; Page 87-88; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human, serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bullimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABK83322-ABK83343 encode human DPRP proteins.
 CC
 XX
 SO Sequence 4159 BP; 894 A; 1306 C; 1174 G; 785 T; 0 other.
 XX
 Alignment Scores:
 Pred. No.: 3,46e-260 Length: 4159
 Score: 2649.00 Matches: 486
 Percent Similarity: 72.89% Conservative: 127
 Best Local Similarity: 57.79% Mismatches: 177
 Query Match: 56.36% Indels: 51
 DB: 24 Gaps: 3
 US-10-070-464-1 (1-882) x ABK83336 (1-4159)
 QY 35 PheTyrValGluArgTyrSerTrpSerGlnLeuAlaLysLeuAlaLysPheArgLys 54
 DB 436 TTCAGAGTGAAGAAGCCTGCGGAGCGGCTCGGAGCATCAACCGAGCGGAG 495
 QY 55 TyrHisGlyTyrMetAlaLysAlaProHisAspPheMetPheValLysArgAsp 74
 DB 496 TACTCGGCGCTCATTTGTCACAAAGGCGCCACGACATTCAGTTTGGCAGAAACGAT 555
 QY 75 ProAspGlyProHisSerAspArgLleTyrTyrLeuAlaMetSerGlyGluAsnArgGlu 94

DB 556 GAGTCTGGGCCCACTCCACCCCTTACTACTGGGATGCCATATGACCGACCGAG 615
 QY 95 AsnThrLeuPheTyrSerGluLleProLysThrLleAsnArgAlaAlaLleuMetLeu 114
 DB 616 AACTCCCTCTCTACTGTGAGATTCCAGAAAGTCCGGAAGACCTCTGCTCTCTG 675
 QY 115 SerTrpLysProLeuLeuAspLlePheGlnAlaThrLeuAspTyrGlyMetTyrSerArg 134
 DB 676 TCCTGGAGACAGATGCTGATTCATTTCCAGGCCACCGCCACCATGGGCTTACTCTCG 735
 QY 135 GluGluGluLeuLeuArgGluArgLysArgLleGlyThrValGlyLleAlaSerTyrAsp 154
 DB 736 GAGAGAGACCTGTGAGGAGGAGAAAGCGCTGGGCTTCCGACATCACTCTACGAG 795
 QY 155 TyrHisGlnGlySerGlyThrPheLeuPheGlnAlaGlySerGlyLleTyrHisValLys 174
 DB 796 TTCACAGCCAGAGTGGCTCTCTCTCCAGCCAGCAACGCTCTTCCACTCTCGCC 855
 QY 175 AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194
 DB 856 GACGCGCGCAAGAACGCTTCATGCTGTCTCCCTATGAACCGCTGAAATCAAGACCCAG 915
 QY 195 CysProAsnLleArgMetAspProLysLeuCysProAlaAspProAspTyrLleAlaPhe 214
 DB 916 TCGTCAGGCGCCCGATGAGACCCCAAAATCTGCTCCGACCTGCTCTCTCTCTC 975
 QY 215 IleHisSerAsnAspLleTyrPheLleSerAsnLleValThrArgGluGluArgLysLeuThr 234
 DB 976 ATCAATTAACAGCAGCTGTGGTGGCCACATCAGACAGCAGGAGCGCGGCTGAC 1035
 QY 235 TyrValHisGlnGluLeuAlaAsnMetGluGluAlaAspLleArgSerAlaGlyValAlaThr 254
 DB 1036 TTCGCGCACCAAGTTTATTCATATGCTCTGATGACCCCAAGTCTGGGGTGGCCACC 1095
 QY 255 PheValLleGlnGluGluPheAspArgTyrSerGlyTyrTyrTyrPyrProLysAlaGlu 274
 DB 1096 TTGCTCATACAGAGAGAGTTCGACCGCTTCACTGGTACTGGTGGTCCACAGCTCC 1155
 QY 275 ThrThrProSerGlyGly---LysLleLeuArgLleLeuArgGluGluAsnAspGluSer 293
 DB 1156 TGGGAGGTTTCAGAGGCTTCAGACCTCGAATCTGTATGAGAGTGCATGATGCTC 1215
 QY 294 GluValGluLleLleHisValThrSerProMetLeuGluThrArgArgAlaAspSerPhe 313
 DB 1216 GAGGTGAGGTCAATTCACGTCCTCCCTCTGCGCTTAAAGAAAGAGAGGATCTGAT 1275
 QY 314 ArgTyrProLysThrGlyThrAlaAsnProLysValThrPheLysMetSerGluLleMet 333
 DB 1276 CGGTACCCCGAGACAGGACAGCAAGAAATCCCAATTCCTTGAACAGCTGAGTTCAG 1335
 QY 334 IleAspLleGluGluArgLleLleAspValLleAspLysGluLeuLleGlnProPheGlu 353
 DB 1336 ACTGACAGCAGGAGGACAGATGCTCGACCCAGAGAGAGAGCTGGTGCACGCTTCAGC 1395
 QY 354 IleLeuPheGluGluValGluTyrLleAlaArgAlaGlyThrProGlnGlyLysTyr 373
 DB 1396 TCGCTGTTCGCAAGAGTGAAGTACATCGCAGGCGGGTGAACCGCGATGCAATATAC 1455
 QY 374 AlaTrpSerLleLeuLeuAspArgSerGlnThrArgLeuGlnLleValLleLleSerPro 393
 DB 1456 GCCTGGGCGATGTCCTGAGACCGGCCCCAGCAGTGGCTCCAGCTCCCTCCCTCCCG 1515
 QY 394 GluLeuPheLleProValGluAspAspValLleGluArgGlnArgLeuLleGluSerVal 413
 DB 1516 GCCCTGTTCATCCGAGACAGAAATGAGAGAGAGGCGGTACCTTCGACAGAGCTGC 1575
 QY 414 ProAspSerValThrProLeuLleLleTyrGluGluThrThrAspLleTyrLleAsnLle 433
 DB 1576 CCCAGAAATTCACCGCGTATGTTGTAGAGAGGTACCAACGTCGTGATCAATGTT 1635
 QY 434 HisAspLlePheHisValPheProGlnSerHis---GluGluGluLleGluPheLlePhe 452


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Db 2090 GCACCCACCCGCTCTTTGTATATGAGAGCCGCCAGGTGACGCTGTAATACCTT 2149
Oy 665 elysglvalylstyphearsleuanshrleuallaserleuglytyvalvalvalva 685
Db 2150 CAAGGCACTACACTTGGCTGAGACACAGCTGGCTCCCTGGGTAGCCCTGTTGT 2209
Oy 685 lileaspaanargglysercyshtsargglyleuulspheluglyalaphelystyry 705
Db 2210 GATTCAGCGGAGGGCTCTGTACAGGAGGGCTGGCTTGAAGGGGCCCTGAAACCA 2269
Oy 705 shetglyglillegliileaspaapclvalgluglyleuglityrleuallaserargty 725
Db 2270 AATGGCCAGCTGAGATGAGAGCAGGCTGAGGCGCTGCACTTGTGCGCCAGAA 2329
Oy 725 rasprheileasprleuapargvalgllylnehslgtyrpsertglytyrleu 745
Db 2330 TGGCTTCATGACCTAGCCGAGGAGCTCCATCCATGGCTGGCTTACGGGGCTCTCTC 2389
Oy 745 rleuMetalaLeuMetGlnargSeraspilrheargvalalalealaglyalprova 765
Db 2390 GCTCATGGGGCTAATCCACAGGCCAGGTTGTCAGAGGTGGCCATGGCGGCTCCCGGT 2449
Oy 765 lhrleutrpilrheargtyrthrclytyrthrgluatgtyrmetglyhisproaspel 785
Db 2450 CACCGCTGATGGCTAGCAGACACAGGCTAACCTGAGCCCTACATGACGCTCCCTGAGAA 2509
Oy 785 nansglngllytyrtyrleuclyservalalameatglnalaglylphrprosergi 805
Db 2510 CAAACGACAGGCTATGAGGGGGGCTCCGTGGCCCTGACAGCTGGAGAAAGCTGCCCATGA 2569
Oy 805 uproAsnargLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 825
Db 2570 GGGCAACGCTGCTATGCTCCAGCGGCTTCCGAGCAAAAGCTCACCTTTTCCACAC 2629
Oy 825 rserlleleuLeuSerRheleuValargalaglylserprotyrAspLeu----- 841
Db 2630 AAACCTCTGCTGCTCCAGACATGATCCGACAGGAAACCTTACACAGCTCCAGGTGGCCT 2689
Oy 842 -----GlnletyrproGlnArguArguHisserlleArgValproGlu 856
Db 2690 GCGCTCTGCTCCGCGGACATGATCCGCAAGAGAGACAGATATGCGCTCCGCGGAGTC 2749
Oy 856 rgluglnlntyrGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 872
Db 2750 GGGCGAGCAGTATGAAGTACAGCTTGTGCACTTGTACAGGAATACCTC 2798

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RESULT 28

ABR83341
ID ABR83341 standard; cDNA; 4037 BP.

AC ABR83341;
XX

DT 12-AUG-2002 (first entry)
XX

DE cDNA encoding human DPP-2 splice variant #9.
XX

Human; serine protease; dipeptidyl peptidase IV-related protein; DPP;
DPP-IV; infection: human immunodeficiency virus; HIV-1; HIV-2; pain;
diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
heart failure; hypertension; urinary retention; osteoporosis; cancer;
ulcer; allergy; cancer; psychiatric disorder; neurological disorder;
dyskinesia; reproductive disorder; inflammatory disorder;
metabolic disorder; gene; ss.
XX

OS Homo sapiens.
XX

PN WO200231134-A2.
XX

PD 18-APR-2002.
XX

PF 12-OCT-2001; 2001WO-US31874.
XX

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PR 12-OCT-2000; 2000US-240117P.
XX
PA (FERR ) FERRING BV.
XX
PI Qi S. Akinsanya KO, Riviere PJ, Junten J:
XX
DR WPI: 2002-444178/47.
XX
P-PSDB: ABR61610.
XX
PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT viral infections, cancers, allergies, neurological disorders, or pain
PT
PS Disclosure: Page 103-104; 113pp. English.
XX
CC The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
CC proteins (DPP). The dipeptidyl peptidase IV-related proteins (DPP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinesias. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABR83332-ABR83343 encode human DPP proteins.
XX
SQ Sequence 4037 BP; 869 A; 1268 C; 1131 G; 769 T; 0 other:

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Alignment Scores:

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Pred. No.: 3,86e-255 Length: 4037
Score: 2599.50 Matches: 479
Percent Similarity: 71.82% Conservative: 125
Best Local Similarity: 56.96% Mismatches: 173
Query Match: 55.31% Indels: 64
DB: Gaps: 4

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US-10-070-464-1 (1-882) x ABR83341 (1-4037)

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Oy 35 pheTyValgluArgtyrserTrpserGlnleuLysleuLeuLlaAsprhArglys 54
Db 436 TTCCAGGTGACAGACACTGCTGGAGCGGCTCCGAGCATCTCCAGGCGACCCGAG 495
Oy 55 tyrHisGlytyrMetalaLysalaProHisAspRheRheRheValLysArgAsp 74
Db 496 TACTCGGCTCATGTGTCAACAGGCGCCGACAGCTTCCAGTTGTGCGAGAGCGAT 555
Oy 75 proAspGlyProHisserAspArgIleTyTyTyTyLeuAlaMetserLylLysAsnArg 94
Db 556 GAGCTGTGGGCCCTGATCCACGCGCTCTACTACTCGGATGCGCATATGCGCCAGAG 615
Oy 95 AsnThrLeuPheTySerGluLeuProLysThrIleAsnArgAlaAlaValleuMetLeu 114
Db 616 AACTGCTCTCTACTCTGATGATTTCCCAAGAGGTCCGGAAGAGGCTCTGCTGCTCTG 675
Oy 115 SerTrpLysProLeuLeuAspLeuPheGlnAlaThrLeuAspTyTyTyTySerArg 134
Db 676 TCTTGAGACAGATGCTGATCTTTCAGAGGCCAGCCGACCATGAGGGGTCTGCTGCG 735
Oy 135 GluGluGluLeuLeuArgGlyAspGlyIleGlyThrValGlyLleLaserTyra 154
Db 736 GAGGAGGAGCTGCTGAGGAGCGGAAAGCGGTGGGTCTTGGCATGCACTCTAGCAC 795
Oy 155 tyrHisGlnGlyserGlyThrPheLeuPheGlnAlaGlySerGlyLleTyThrHisVal 174
Db 796 TTCCACAGGAGAGGTGGCTTCTCTTCCAGGCGAGCAAGCGCTCTTCCAGCTCCGCG 855
Oy 175 AspGlyGlyProGlnIlyPheThrGlnGlnProLeuArgProAsnLeuValGluThrSer 194

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Db	856	GAGGGCGGCAAGAACGGCTTCATGTGTCCCTCATATGAACCGCTGGAATCAAGCCAG	915
Qy	195	CysProasnIleArgMetAspProLysLeuCysProAlaAspProAspTrpIleAlaPhe	214
	111		:::
Db	916	TTCCTAGAGGCCCCGGATGGAGACCCCAAAATCTGCCCTTCCGAGACCTTCCTTCCTTC	975
Qy	215	IleHisSerAsnAspIleTrpIleSerAsnIleValThrArgLysLysIleValThrArg	234
Db	976	ATCAATTAACACGCGACTGTGGGTGGCCACATGGAGAACGGCAGAGACGGCGCTGAC	1035
Qy	235	TyrValHisAsnGluLeuAlaAsnMetGluLysAspAlaSerLysIleValThrArg	254
	:::		:::
Db	1036	TTCCTCCACCAAGGTTTATTCATATGTCTTGATGACCCCAAGTCGTGGGTGGCCAC	1095
Qy	255	PheValLeuGluGluGluIlePheAspArgTyrSerGlyTyrTrpTrpCysProLysAla	274
Db	1096	TTCGTCATACAGGAAGAAGTTCCAGCCCTTCACGTGGGTACTGGGTGGCCACACCTTC	1155
Qy	275	ThrTrpProSerGlyGly---LysIleLeuArgIleLeuTyrGluLysAsnAspLys	293
Db	1156	TGGGAAGGTTCCAGAGGGGCTTCAGAACCTCTCGAATCTGTAGAGGAATCATCATGTC	1215
Qy	294	GluValIleGluIleHisValThrSerProMetLeuGluThrArgArgLysAspSer	313
Db	1216	CAGGTGGAGGTTCATTCACGTCCCTCTCCGTGAAAGAAAGGAAGACGGACTCGAT	1275
Qy	314	ArgTyrProLysTrpGlyTyrThrAlaAsnProLysValThrPheLysMetSerGluIle	333
Db	1276	CGGTATCCCGACAGAGCAGCAGCAAGAAATCCCAAGATTGGCTTGAACCTGCTGATTCC	1335
Qy	334	IleAspAlaGluGlyArgIleIleAspValIleAspLysGluLeuIleGlnProPhe	353
Db	1336	ACTGACACCCAGGGCCAGAGTCGTCCGACCCAGGAAGAAGAGCTGTGTGACGCTTCAG	1395
Qy	354	IleLeuPheGluGlyValGlyTyrIleAlaArgAlaGlyTrpTrpProGluLysTyr	373
Db	1396	TGCGTGTCCCGAAGGTGGAGTACATGCTCCAGGGCCGGGTGGACCCGGATGCAATAC	1455
Qy	374	AlaTrpSerIleLeuLeuAspArgSerGlnThrArgLeuGlnIleValLeuIleSerPro	393
Db	1456	GCTTGCGGCAATGTTCTGGAGACGGGCCACAGAGGTGCTCAGCTGCTCTCCCTCC	1515
Qy	394	GluLeuPheIleProValGluAspAspValMetGluArgGlnArgLeuIleGluSerVal	413
Db	1516	GCCCTGTTCAATCCGACACAGAAAGAGAACACCGCTACGCTCCAGACCTGTC	1575
Qy	414	ProAspSerValThrProLeuIleIleTyrGluGluThrThrAspIleTrpIleAsnIle	433
Db	1576	CCGAGGATGTCCAGCCGCTATGTGTGTACAGAGAGGTCAACACGCTGTGATCATGTT	1635
Qy	434	HisAspIlePheHisValPheProGlnSerHis---GluGlnGluIleGluPheIlePhe	452
Db	1636	CATGCAATCTTCTATCCCTTCCCCCAATGAGGAGAGAGACGATGCTTCTCCGC	1695
Qy	453	AlaSerGlyCysLysTrpGlyPheArgHisLeuTyrLysIleThrSerIleLeuLysGlu	472
Db	1696	GCCATGTATCAAGAACCGGCTTGTGCATTGTACAAAGTCAACCCGCTTTAAATAAC	1755
Qy	473	SerLysTyrLysArgSerSerGlyLysLeuProAlaProSerAspPheLysGlySerPro	492
Db	1756	CAGGCTACGATGGAGTGAACCTTCAGCCCGGGGAAGATGAATTAAAGTCCCATTT	1815
Qy	493	LysGluGluIleAlaIleThrSerGlyLysTrpGluValLeuGluValArgHisLysSerAsn	512
Db	1816	AAGGAGAGATTTGCTGTGACACAGGGATGGAGATTTTGGCAGGACGACGCTC---	1872
Qy	513	IleGlnValAspGluValArgArgLeuValTyrPheGluGluLysThrLysAspSerPro	532
Db	1873	-----AAGGCAACCAAGACACGCGCTG	1896
Qy	533	GluHisHisLeuTyrValValSerTyrValAsnProGlyGluValThrArgLeuThrAsp	552
Db	1897	GAGCAACACCTTACGTGTGACGTATGAGCGCGCGGAGAGTCTGTACGCTTCACAG	1956

QY	553	ArgGIyIYrSerHISserCysCIleSerGlnHIScysAspPhePheIleSerLysIYr	572
Db	1957	CCCCGCTTCTCCATACCTACTCTCTCCATGAGCCAAACCTTCGACATGTTCGTGACACCATAC	2016
QY	573	SerAsnGlnLysAsnProHIScysValSerLeuTYrLYsLeuSerSerProGlnAspasp	592
Db	2017	AGCAGCGGAGACACGCCGCCCTCGTGCACAGCTCTACAAAGCTAGAGGGGCCCGACGACAC	2076
QY	593	ProThrCysLysThrLYsGlnPheTrpAlaThrIleLeuAspSerAlaGlyProLeuPro	612
Db	2077	CCCCGACAAAGCAGCCCCCTCTGTGGCGTAGCATGATGAGGACGACGAGCTGCCCCCG	2136
QY	613	AspTYrThrProProGlnIlePheSerPheGlnSerThrThiGlyPheThrLeuTYrGly	632
Db	2137	GATTATGTCCTCCAGAGATCTTCACATTCACACCGCGCTCGGATGCGGCTCTACGGC	2196
QY	633	MetLeuTYrLYsProHISAspLeuGlnProGlyLYsLYsTYrProThrValLeuPheIle	652
Db	2197	ATGATCTTACAGCCCCCAGCGCTTGCAGCCAGGAAAGAACACCCACCGCTCTCTTGTGA	2256
QY	653	TYrGlyGlyProGlnValGlnLeuValAsnAsnArgPheLYsGlyValLYsTYrPheArg	672
Db	2257	TATGAGAGCCCCCGAGCGAGCTGTGGAATATCTTCCTTAAAGCATACATACACTTCGGG	2316
QY	673	LeuAsnThrLeuAlaSerLeuGlyTYrValValValIleAspAsnArgGlySerCys	692
Db	2317	CTCACACACATCGGCTCTCCCTGGGCTACGCCCGTGTGTATTTAGACGACGAGGGCTCTCT	2376
QY	693	HISArgGlyLeuLYsPheGlnGlyAlaPheLYsTYrLYsMetGlyGlnIleGlnLeuAsp	712
Db	2377	CAGGAGGCTTCGTTCCGTCGAAGGGCCCTCGAATAACCAATATGGCCAGAGTGGAGTGCAG	2436
QY	713	AspGlnValGlnGlyLeuGlnTYrLeuAlaSerArgTYrAspPheIleAspLeuAspArg	732
Db	2437	GACCAAGGAGGAGGCGCTCGAGTTCTGTGCCGAGAACTATGAGCTCATGACCTTAGCGCGA	2496
QY	733	ValGlyIleHISGlyTYrSerTYrGlyGlyTYrLeuSerLeuMetAlaIleuMetGlnArg	752
Db	2497	GTTGGCATTCATGGCTGTGCTCTACAGGGGCTTCCTCTCGCTCATGTGGGCTAATCCACAG	2556
QY	753	SerAspIlePhe-ArgValAlaIleAlaGlyAlaProValThrLeuTrpIlePheTYrAs	772
Db	2557	CCCCAGGCTTCCAGG-----	2572
QY	772	PTHGlyTYrThrGlnArgTYrMetGlnHISProAspGlnAsnGlnGlnGlyTYrTYrLe	792
Db	2572	-----	2572
QY	792	uGlySerValAlaMetGlnAlaGlnLYsPheProSerGlnProAsnArgLeuLeuLeu	812
Db	2573	-----CCCAACCGCTTGCTTATCT	2592
QY	812	uHISGlyPheLeuAspGlnAsnValHISpheAlaHISThrSerIleLeuLeuSerPheLe	832
Db	2593	CCAGCGGCTTCTGTGACCAAAACSTGTGACTTTTCCACAAACCTTCGTCGTCCCACT	2652
QY	832	uValArgAlaGlyAspProTYrAspLeuGlnIleTYrProGlnGlnuArgHISSerIleAr	852
Db	2653	GATCCGAGCAGGAAACCTTACCAAGCTCCAGATCTAACCCCAACGAGAGACACAGATTTCG	2712
QY	852	gValProGlnSerIleLYsGlnHISTYrGlnLeuHISLeuHISLeuHISTYrLeuGlnGlnLys	872
Db	2713	CTGGCCCGAGTGGGCGAGACATGACAGTACAGCTGTGCTGCACTTTCTACAGGAATACT	2772
QY	872	u 872	
Db	2773	C 2773	
RESULT 29			
ID ABR83340 standard; cDNA; 4120 BP.			
XX			

AC		ABR83340;			
xx					
DI		12-AUG-2002	(first entry)		
DE		cDNA encoding human DPRP-2 splice variant #8.			
xx					
KW		Human: serine protease; dipeptidyl peptidase IV-related protein; DPPRP; DPPRV; infection; human immunodeficiency virus; HIV-1, HIV-2, pain, diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke; heart failure; hypertension; urinary retention; osteoporosis; cancer; KM allergy; cancer; psychiatric disorder; neurological disorder; dyslexia; reproductive disorder; inflammatory disorder; metabolic disorder; gene; ss. KW XX			
OS		Homo sapiens.			
PN		MO2002j1134-A2.			
PD					
xx		18-APR-2002.			
PF		12-OCT-2001; 2001WO-US31874.			
PR		12-OCT-2000; 2000US-240117P.			
PA		(FERR) FERRING BV.			
Pt		Qi S, Akinsanya KO, Riviere PJ, Junien J:			
DR		WPI: 2002-444178/47.			
xx		P-PsDB: ABR61609.			
Pt		New dipeptidyl peptidase IV-related proteins and nucleic acids encoding			
Pt		the proteins, useful for treating e.g. fungal, bacterial, protozoan and			
PT		viral infections, cancers, allergies, neurological disorders, or pain			
PS		-			
xx					
Dis		Disclosure: Page 100-101; 113pp; English.			
CC		The present invention relates to the isolation of novel human serine			
CC		proteases referred to as dipeptidyl peptidase IV (DPPIV)-related			
CC		proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)			
CC		and nucleic acids encoding them are useful for treating infections			
CC		such as fungal, bacterial, protozoan and viral infections, particularly			
CC		infections caused by human immunodeficiency virus (HIV-1 or HIV-2),			
CC		pain, diabetes, precocious puberty, infertility, obesity, anorexia,			
CC		bulimia, Parkinson's disease, acute heart failure, hypotension,			
CC		hypertension, urinary retention, osteoporosis, angina pectoris,			
CC		stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,			
CC		psychotic and neurological disorders (e.g. anxiety, dementia, or			
CC		schizophrenia), and dyslexias. These may also be used in discovering			
CC		therapeutic agents for the treatment of reproductive, inflammatory and			
CC		metabolic disorders. ABR83322-ABR83343 encode human DPPR proteins.			
xx					
SQ		Sequence 4120 BP; 884 A; 1298 C; 1162 G; 776 T; 0 other;			
Alignment Scores:					
Pred. No.: 3 98E-255		Length: 4120			
Score: 2599.50		Matches: 479			
Percent Similarity: 71.82%		Conservative: 125			
Best Local Similarity: 56.96%		Mismatches: 173			
Query Match: 55.31%		Indels: 64			
DB: 24		Gaps: 4			
US-10-070-464-1 (1-882) x ABR83340 (1-4120)					
OY		35 PheTYrValGIuAlaTyrSerTrpSerGlnLeuLysIleuLeuAlaAspThrArgLys 54			
Db		: :: ::			
		436 TTCCAGTGCGCAAGAACAACACTCCTGGGGAAGCGGCCTCCGAGCATATCACGCCAGCCCCAACG 495			
OY		55 TyrHisGLyTYrMetCMeTAlysaLaProHisAspPhemctPheValLysArgnaSp 74			
Dz		:			
		496 TACTGTGGGCTTCATTGTGTCAACAAGCGCGCCCAGACTTCCAATTTGTGTGCAAGAAGCGAT 555			

QY	75	ProAspSgLYProHisSerAspArgLYleTYrTYrLeuAlaMetSerGlyGluAsnArgGlu	94
Db	556	GAGTCGTGGGCCCCCCTCCACCGCCCTTACTACTCGGAATGCATATGCGACCGCGAAG	615
QY	95	AsnThrLeuPheTYrSerGluIleProLYsThrILeAsnArgAlaValaLeuMetLeu	114
Db	616	AACTCCTCCCTCTACTGTGAGATTCCCAAGAGGTCCGGAAGAGGCTCTGCTGCTCTG	675
QY	115	SerTYrLYsProLeuLeuAsnProPheGlnAlaThrLeuAspTYrGlyMetTYrSerArg	134
Db	676	TCTGTGAAGCAGATGCTGTGATCATTTTCCAGGCCACGCCACCACATGTGGGTCTACTCTGG	735
QY	135	GluGluGluLeuLeuArgGluArgLYsArgLYleGlyThrValGlyLYleAlaSerTYrAsp	154
Db	736	GAGGAGGAGCTGCTGAGGAGCGGAACCGCTGGGGGTCTTGGGCTACCTCTCAAGAC	795
QY	155	TYrHisGlnGlySerGlyTYrThrPheLeuPheGlnAlaGlySerGlyLYleThrHisValys	174
Db	796	TTCCACACCGAGATGGCTCTTCTCTTCCAGGCCACGAACGCTCTTCCACTGCGGC	855
QY	175	AspGlyGlyProGlnGlyPheThrGlnGlnProLeuArgProAsnLeuValaGluThrSer	194
Db	856	GACGGCGGCAGAACGGGCTTCATGTGTCTCCCTATGAACCGCTGGAATCAAGACCGAG	915
QY	195	CysProAsnLYleArgMetAspProLYsLeuCysProAlaAspProAspTYrIleAlaPhe	214
Db	916	TGCTCAGCGCCCGGATGGAGCCCAAAATGTCCCTCGCGAGCCCTCTCTTCTCTTCC	975
QY	215	IleHisSerAsnAspIleTYrIleSerAspLYleValaThrArgGlnGluArgArgLeuThr	234
Db	976	ATCATATTAACACCGACCTGTGGGTGGCCAACTAGACAGACGCGAGGCGCGCTGAC	1035
QY	235	TYrValIleAsnGlnLeuAlaAsnMetGlnLYsAlaPalaArgSerAlaGlyValaIleThr	254
Db	1036	TTTGTGCACCAAGGTTTATTCATATGTCTGTGATGAGCCCAAGTCTCGGGTGTGGCCAC	1095
QY	255	PheValLeuGlnGluGluPheAspArgTYrSerGlyTYrTYrTYrTYrProLYsAlaGlu	274
Db	1096	TTTCGTACATACAGGAAGATTCTGCACCGCTTCACTGCGGTACTGGGTGGCCCAACCTTC	1155
QY	275	ThrThrProSerGlyGly---LYsIleLeuArgIleLeuTYrGlnGluAsnSgLYser	293
Db	1156	TGGCAGAGTTCTAGAGGCTCTCAAGCCGTCAAGCCTGTATATGAGAACTCATATGATCC	1215
QY	294	GluValGluIleIleHisValaThrSerProMetLeuGluThrArgArgAlaSerPhe	313
Db	1216	GAGGTGAGAGTCATTCAACGTCCTCCCTCCGCGCTGAGAAAGAAAGAACGGAATCTGAT	1275
QY	314	ArgTYrProLYsThrGlyTYrThrAlaAsnProLYsValaTYrPheLYsMetSerGluIleMet	333
Db	1276	CGGTATCCCCACAGACGAGCAGACAGAAATCCCAAGATTGCCCTTGAACTGCTGATTTCCAG	1335
QY	334	IleAspAlaGluGlyArgGlyIleIleAspValaIleAspLYsGluLeuIleGlnProPheGlu	353
Db	1336	ACTGACACCCGAGGGCAGATCTGTCTCCACCGAAGAAAGAGCTGTGTGACGCCCTTTCAGC	1395
QY	354	IleLeuPheGlnGlyValaGlyTYrTYrIleAlaArgAlaGlyTYrThrProGlnLYsTYr	373
Db	1396	TGCGCTTTCCGAGAGTGAGATCATGTCCACGGGCCGGGTGGACCCGGATGGAATATAC	1455
QY	374	AlaTYrSerIleLeuLeuAsnArgSerGlnTYrArgLeuGlnIleValaLeuIleSerPro	393
Db	1456	GCTGTGGCCATGTCCTTGAGACCGGCCACACAGTGTGCTCAGATGTCCTCTCCGCCCG	1515
QY	394	GluLeuPheIleProValaGluAspAspValaMetGluArgGlnArgLeuIleIleSerVal	413
Db	1516	GCCCTGTTCATCCCGACACAGAAATGAGACGACACCGGCTAGCCTTCCAGACTGTGC	1575
QY	414	ProAspSerAlaThrProLeuIleIleTYrGlnGlyThrThrAspIleTYrIleAsnIle	433
Db	1576	CCCAAGATGTCCAGCGCTATGTGTGTACAGAGAGGTCAACCAAGTCTGGATTCATGTT	1635
QY	434	HisAspIlePheHisValaPheProGlnSerHis--GluGluGluIleGluPheIlePhe	452

[illegible]

Db	2573	-----CCCAACCGCTGCTTACT	2592
Qy	812	uHISGLYPheLeuAspGLuaSNValHisPhealHisIstRSerLleLeuLeuSerPhe	832
Db	2593	CCACGGCTTCCTCGACCAAAACCTGCACCTTTTCCACCAAACTTCGCTCCCAACT	2652
Qy	832	uValAlaAlaGLYAspProGlyrasPleuGlnIleTyRProGlnGlnuATGHisSerLleAr	852
Db	2653	GATCCGAGCAGGGAACCTTACACAGCTCCAGAGCTACCCCAACGAGAGACAGATTTCG	2712
Qy	852	gValIProGLISerGLYAspIleHisTyRGLueuHisLeuLeuHisTyRLeuGlnGLuaSnle	872
Db	2713	CTGCGCCGAGTGGGCGACGACATCATAGTACACGTTGCGCAGCTTTCTACAGGATTACT	2772
Qy	872 u 872		
Db	2773 C 2773		
RESULT: 30			
AI57880			
ID	AI57880	standard; cDNA: 3262 BP.	
AC	AI57880;		
XX	22-OCT-2001	(first entry)	
DE	Human polynucleotide SEQ ID NO 83.		
XX			
KW	Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;		
XX	Leukemia; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200153312-A1.		
XX			
PD	26-JUL-2001.		
XX			
PE	26-DEC-2000; 2000MO-US34263.		
XX			
PR	21-JAN-2000; 2000US-0488725.		
PR	25-APR-2000; 2000US-0552317.		
PR	09-JUL-2000; 2000US-0598042.		
PR	19-JUL-2000; 2000US-0620312.		
PR	03-AUG-2000; 2000US-0653450.		
PR	14-SEP-2000; 2000US-0662191.		
PR	19-OCT-2000; 2000US-0693036.		
PR	29-NOV-2000; 2000US-0727344.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
FI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;		
PI	Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;		
PI	Zhao QA, Zhou P, Goodrich R, Dirmann RT;		
XX			
DR	.WPI: 2001-442253/47.		
XX	P-PSDB; AAM38724.		
PT	Novel nucleic acids and polypeptides, useful for treating disorders		
PT	such as central nervous system injuries -		
XX			
PS	Claim 1; SEQ ID NO 83; 10078bp; English.		
XX			
CC	The invention relates to human nucleic acids (AI57798-AI61369) and		
CC	the encoded polypeptides (AAM38642-AAM42213) with nocotropic,		
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful		
CC	in gene therapy. A composition containing a polypeptide or polynucleotides		
CC	of the invention may be used to treat diseases of the peripheral nervous		
CC	system, such as peripheral nervous injuries, peripheral neuropathy and		
CC	localised neuropathies and central nervous system diseases, such as		

[illegible]


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PR 18-FEB-2000; 2000AU-0005709.
XX
XX (UNSY ) UNIV SYDNEY.
XX
PI Abbott CA, Gorell MD;
XX
XX WPI; 2001-281520/29.
DR N-PSDB; AAC85694.
XX
PT New human dipeptidyl aminopeptidase (DPP8) useful for cleaving
PT substrates, identifying inhibitors of DPP8 catalytic activity which
PT have therapeutic uses, and for detecting activated T cells
XX
XX Claim 1; Fig 2; 78pp; English.
XX
CC This sequence represents human dipeptidyl aminopeptidase (DPP8).
CC DPP8 has substrate specificity for H-Ala-Pro-PNA, H-Gly-Pro-PNA and
CC H-Arg-Pro-PNA. Therefore, it is a prolyl oligopeptidase and a
CC dipeptidyl peptidase, because it is capable of hydrolysing the
CC peptide bond C-terminal to Pro in each of these compounds. DPP8
CC is homologous with human DPPiv. DPP8 is useful for cleaving a
CC substrate, and for detecting an activated T cell which involves
CC measuring the level of DPP8 gene expression in a T cell. The level
CC of DPP8 expression is detected by detecting the amount of DPP8 RNA
CC in the cell. It is also useful for identifying a molecule capable
CC of inhibiting the cleavage of the substrate by DPP8. Molecules
CC identified as inhibiting DPP8 catalytic activity may be useful for
CC treating diarrhoea, growth hormone deficiency, lowering glucose levels
CC in non-insulin dependent diabetes mellitus and other disorders
CC involving glucose intolerance, enhancing mucosal regeneration and
CC as immunosuppressants.
XX
XX Sequence 882 AA;
SQ
Query Match 100.0%; Score 4700; DB 22; Length 882;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAMETEQLEVEIFETADCEENIESODRPLEPFYERYYSWSOLKLLADTRKHGYMM 60
DB 1 MAAMETEQLEVEIFETADCEENIESODRPLEPFYERYYSWSOLKLLADTRKHGYMM 60
QY 61 AKAPHEMFYKRNPDGPHSDRIYYLAMSGENRENTLFYSIPTINRAVALMSKPL 120
DB 61 AKAPHEMFYKRNPDGPHSDRIYYLAMSGENRENTLFYSIPTINRAVALMSKPL 120
QY 121 DLFOATLDYGYMSREELLRKRKIGTVGASDYHOGSGFELFOAGSGIYHVRDGGPQG 180
DB 121 DLFOATLDYGYMSREELLRKRKIGTVGASDYHOGSGFELFOAGSGIYHVRDGGPQG 180
QY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSDNIIWISNIVTREERLTYVHNL 240
DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDWIAFIHSDNIIWISNIVTREERLTYVHNL 240
QY 241 ANMEEDARSAGVATFYQEEFDRISGYWCKAKETTPSGKILRLIYENDESEVEIIVH 300
DB 241 ANMEEDARSAGVATFYQEEFDRISGYWCKAKETTPSGKILRLIYENDESEVEIIVH 300
QY 301 TSPLETRRADSFYRPTGTANPKVTFKMSFIMIDAGRIIDVIDKELIOFELLFSGVE 360
DB 301 TSPLETRRADSFYRPTGTANPKVTFKMSFIMIDAGRIIDVIDKELIOFELLFSGVE 360
QY 361 YIARAGWTEGKYAWMSILDRSOTRLOIVLISPELFIPEVDVVERORLIESVPDSVPL 420
DB 361 YIARAGWTEGKYAWMSILDRSOTRLOIVLISPELFIPEVDVVERORLIESVPDSVPL 420
QY 421 IYIETTDIWNIDIRHVPOSHHEELIEFPAECKTGFFHLKYITSLKESYKRSNG 480
DB 421 IYIETTDIWNIDIRHVPOSHHEELIEFPAECKTGFFHLKYITSLKESYKRSNG 480
QY 481 GLPAPSDFKCPKEIKAITSGEWEVLGRHGSNIQVDEVRRLIYVEGTRKDSLEHLLVVS 540
DB 481 GLPAPSDFKCPKEIKAITSGEWEVLGRHGSNIQVDEVRRLIYVEGTRKDSLEHLLVVS 540

```

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QY 541 YVNGEYTRLDRCYSHSCISQHCDFEISKYSNOKNPHCYSLYKLSPPDDPTCKTEF 600
DB 541 YVNGEYTRLDRCYSHSCISQHCDFEISKYSNOKNPHCYSLYKLSPPDDPTCKTEF 600
QY 601 WATILDSAGPLPDYTPPEIFSESTGTLYGMLYKPHDLQPKKPYTLFIYGGPOVL 660
DB 601 WATILDSAGPLPDYTPPEIFSESTGTLYGMLYKPHDLQPKKPYTLFIYGGPOVL 660
QY 661 VNNRFKGVKFRNLTLASLSGVVYVINDRSGCHGKLFEGAFKKMQIETDQVELOY 720
DB 661 VNNRFKGVKFRNLTLASLSGVVYVINDRSGCHGKLFEGAFKKMQIETDQVELOY 720
QY 721 LASRYDEFLDRVGIHGSYGYLSLMAQMORSDFPVAIAGAPVTLMITFDGTYERYM 780
DB 721 LASRYDEFLDRVGIHGSYGYLSLMAQMORSDFPVAIAGAPVTLMITFDGTYERYM 780
QY 781 GHPDQNEGYLYGSVAMQAEKFPSEPNRLLHGFEDENVHFAHTSILSFLYRAGKPYD 840
DB 781 GHPDQNEGYLYGSVAMQAEKFPSEPNRLLHGFEDENVHFAHTSILSFLYRAGKPYD 840
QY 841 LQIYPOERHSTRPESEGEHELHLHYLOENLGSRIALKVI 882
DB 841 LQIYPOERHSTRPESEGEHELHLHYLOENLGSRIALKVI 882
RESULT 2
AAE24170
ID AAE24170 standard; Protein; 882 AA.
XX
XX AAE24170;
XX
XX 23-SEP-2002 (first entry)
XX
DE Human dipeptidyl peptidase 8 (DPP8) protein.
XX
XX Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
XX autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
XX KW graft rejection; anti-diabetic; anti-inflammatory; immunosuppressive;
XX KM antiviral; enzyme.
XX
XX Homo sapiens.
XX
XX WO200234900-A1.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-A001388.
XX
XX 27-OCT-2000; 2000AU-0001078.
XX
XX (UNSY ) UNIV SYDNEY.
XX
PI Abbott CA, Gorell MD;
XX
XX WPI; 2002-454646/48.
XX
XX N-PSDB; AAD38956.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening
PT inhibitors of DPP catalytic activity, which may be employed to treat
PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
PT rejection and HIV infection -
XX
XX Example; Fig 1; 91pp; English.
XX
XX The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX CC polynucleotides encoding such proteins. The DPP peptides are useful for
XX CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX CC rejection and HIV (human immuno deficiency virus) infection. The present
XX CC sequence is human DPP8 protein.
XX
XX Sequence 882 AA;
SQ

```

Query Match 100.0%; Score 4700; DB 23; Length 882;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMETBOLGVEIFETADCEENIESODRKLPEFVERYSWSQKLLADTRKRYGYM 60
 DB 1 MAAMETBOLGVEIFETADCEENIESODRKLPEFVERYSWSQKLLADTRKRYGYM 60

QY 61 AKAPHFMEFKRNDPDPGPHSDRIYIYLAAMSGENRENTLFYSEIKTINRAVLMLSKPLL 120
 DB 61 AKAPHFMEFKRNDPDPGPHSDRIYIYLAAMSGENRENTLFYSEIKTINRAVLMLSKPLL 120

QY 121 DLFQATLDYGMYSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180
 DB 121 DLFQATLDYGMYSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180

QY 181 FTQOPLRPNLVETSCNIRNDPKLCPADPDWIAFIHNSNDIWSNIYTRERRLTYVHNEL 240
 DB 181 FTQOPLRPNLVETSCNIRNDPKLCPADPDWIAFIHNSNDIWSNIYTRERRLTYVHNEL 240

QY 241 ANNEEDARSAGVATFVLOEEFDRTSGYMWCPKAKETTPSGKILRLIYEENDESEVEIHY 300
 DB 241 ANNEEDARSAGVATFVLOEEFDRTSGYMWCPKAKETTPSGKILRLIYEENDESEVEIHY 300

QY 301 TSPMLTERRADSFRRYKGTGTANKVTFKMSIEMIDAGRIIDYIDKELIQPEILFEGVE 360
 DB 301 TSPMLTERRADSFRRYKGTGTANKVTFKMSIEMIDAGRIIDYIDKELIQPEILFEGVE 360

QY 361 YIARAGMTEBGKXAMSIILDRSOTRQIYLISELFIPEDDVMERORLIESVPSDTPPL 420
 DB 361 YIARAGMTEBGKXAMSIILDRSOTRQIYLISELFIPEDDVMERORLIESVPSDTPPL 420

QY 421 IYEEETDWINHDIHFVPOSHHEIEFIASECKTGRIHYKTSILKESKVRSSG 480
 DB 421 IYEEETDWINHDIHFVPOSHHEIEFIASECKTGRIHYKTSILKESKVRSSG 480

QY 481 GLPAPSDFCPIKEEIAITSGEWEVLGRHNSIQVDEVRLYVEFGTKSPLEHHLVYVS 540
 DB 481 GLPAPSDFCPIKEEIAITSGEWEVLGRHNSIQVDEVRLYVEFGTKSPLEHHLVYVS 540

QY 541 YVNRGEVTLTDGYSHSCCISCHCPFIISKYSNOKNPHCVSLKISSPEDDCTKTER 600
 DB 541 YVNRGEVTLTDGYSHSCCISCHCPFIISKYSNOKNPHCVSLKISSPEDDCTKTER 600

QY 601 MATILDSAGPLPYTPPEIFSFESTGTGTLGMLYKPHDQPGKATPYVLFITGSGVOYL 660
 DB 601 MATILDSAGPLPYTPPEIFSFESTGTGTLGMLYKPHDQPGKATPYVLFITGSGVOYL 660

QY 661 VNNRFKGVKFRNLNTLASLGYVVVIDNNGSCHRGKLFEGAFKRYKMGQIEIDQVEGLQY 720
 DB 661 VNNRFKGVKFRNLNTLASLGYVVVIDNNGSCHRGKLFEGAFKRYKMGQIEIDQVEGLQY 720

QY 721 LASRYFIDLDKRGHIGWSTGYLSLMAIMQNSDIFRVAIAGPVLWTFYDTGYERYM 780
 DB 721 LASRYFIDLDKRGHIGWSTGYLSLMAIMQNSDIFRVAIAGPVLWTFYDTGYERYM 780

QY 781 GHDDONEGCGYIGSVAMQAEKFPSEPNRLLLHGFIDENVFAHTSLLISFLVRACKPYD 840
 DB 781 GHDDONEGCGYIGSVAMQAEKFPSEPNRLLLHGFIDENVFAHTSLLISFLVRACKPYD 840

QY 841 LQIYPOERHSIRVSEGEHEHLHLHYLOENLGSRTAALKVI 882
 DB 841 LQIYPOERHSIRVSEGEHEHLHLHYLOENLGSRTAALKVI 882

RESULT 3
 ABG61591
 ID ABG61591 standard; Protein: 882 AA.
 XX
 AC ABG61591;
 XX
 DT 12-AUG-2002 (first entry)

XX DE Human DPPIV related serine protease DPP-1.
 XX KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPPP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.
 XX KW
 XX OS Homo sapiens.
 XX PN W0200231134-A2.
 XX PD 18-APR-2002.
 XX PF 12-OCT-2001; 2001WO-US31874.
 XX PR 12-OCT-2000; 2000US-240117P.
 XX PA (FERR) FERRING BV.
 XX PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
 XX DR WPI; 2002-444178/47.
 XX N-PSDB; ABK83322.
 XX PT New, dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 XX
 XX Claim 17; Fig 1; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
 XX
 XX Sequence 882 AA:
 SQ

Query Match 100.0%; Score 4700; DB 23; Length 882;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMETBOLGVEIFETADCEENIESODRKLPEFVERYSWSQKLLADTRKRYGYM 60
 DB 1 MAAMETBOLGVEIFETADCEENIESODRKLPEFVERYSWSQKLLADTRKRYGYM 60

QY 61 AKAPHFMEFKRNDPDPGPHSDRIYIYLAAMSGENRENTLFYSEIKTINRAVLMLSKPLL 120
 DB 61 AKAPHFMEFKRNDPDPGPHSDRIYIYLAAMSGENRENTLFYSEIKTINRAVLMLSKPLL 120

QY 121 DLFQATLDYGMYSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180
 DB 121 DLFQATLDYGMYSREBELLRERKRIGTVGIASDYHOGSGTFLEQAGSGIYHVKDGPQG 180

QY 181 FTQOPLRPNLVETSCNIRNDPKLCPADPDWIAFIHNSNDIWSNIYTRERRLTYVHNEL 240
 DB 181 FTQOPLRPNLVETSCNIRNDPKLCPADPDWIAFIHNSNDIWSNIYTRERRLTYVHNEL 240

QY 241 ANNEEDARSAGVATFVLOEEFDRTSGYMWCPKAKETTPSGKILRLIYEENDESEVEIHY 300

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|||||
Db 241 ANNEEDARSAGVATFVLOEEFDRSGYWCMPKATETPSGKILRLILEENDESEVEIHH 300
QY 301 TSPMLETRRADSPFRYPKGTANPKVTFKMSIIMDAGRIIIVDKLQPFELFEGVE 360
Db 301 TSPMLETRRADSPFRYPKGTANPKVTFKMSIIMDAGRIIIVDKLQPFELFEGVE 360
QY 361 YIARAGTPEGKYAMSIILDRSOTRLOIVLISPELFPVEDDWERORLIESVDSYTPL 420
Db 361 YIARAGTPEGKYAMSIILDRSOTRLOIVLISPELFPVEDDWERORLIESVDSYTPL 420
QY 421 IYEEETDWINIHDIHFVFPQSHHEEIEFIFASECTGRHLKITSILKESYKRSSG 480
Db 421 IYEEETDWINIHDIHFVFPQSHHEEIEFIFASECTGRHLKITSILKESYKRSSG 480
QY 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNIQVDEVRLVYFEGTKDSPLEHHLVVS 540
Db 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNIQVDEVRLVYFEGTKDSPLEHHLVVS 540
QY 541 YVNPGEVTRLDRGYSHSCCISOHCDEFISKYSNQNPKHCVSLKLSPEDDPTCKTEF 600
Db 541 YVNPGEVTRLDRGYSHSCCISOHCDEFISKYSNQNPKHCVSLKLSPEDDPTCKTEF 600
QY 601 WATILDSAGLPDYTPPEITFSESTGFTLYGMLYKPHDLOPKKYPVLFYIGPQVOL 660
Db 601 WATILDSAGLPDYTPPEITFSESTGFTLYGMLYKPHDLOPKKYPVLFYIGPQVOL 660
QY 661 VNNFEKGVKFRLLNTLASLGVVVVINDRSGCHRLKFECAFYKFKMOIIEDDOVEGLQY 720
Db 661 VNNFEKGVKFRLLNTLASLGVVVVINDRSGCHRLKFECAFYKFKMOIIEDDOVEGLQY 720
QY 721 LASRYDEIDLDVAGIHGMSYGGYLSLMAQMORSIDIFRVAIAGAVTLWIFDYGTERYM 780
Db 721 LASRYDEIDLDVAGIHGMSYGGYLSLMAQMORSIDIFRVAIAGAVTLWIFDYGTERYM 780
QY 781 GHPOONOGYVLGSVMAQAEKFPSEPNRLILLHGFLENNHFAITSLILSTLVAGRPYD 840
Db 781 GHPOONOGYVLGSVMAQAEKFPSEPNRLILLHGFLENNHFAITSLILSTLVAGRPYD 840
QY 841 LQIYPERHSIRVPESEGEHELHLHLEMLGSGRIALAKYI 882
Db 841 LQIYPERHSIRVPESEGEHELHLHLEMLGSGRIALAKYI 882

RESULT 4
AAU74749
ID AAU74749 standard; Protein: 882 AA.
XX
AC AAU74749;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protease PR7S-9 protein sequence.
XX
KW Human; protease; PR7S; gastrointestinal; Crohn's disease; cancer;
KW cardiovascular; atherosclerosis; autoimmune disorder; dermatitis;
KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KW cell proliferative disorder; developmental disorder; epilepsy;
KW Duchenne muscular dystrophy; epithelial disorder; neurological disorder;
KW reproductive disorder; endometriosis.
XX
OS Homo sapiens.
XX
PN MO200198468-A2.
XX
PD 27-DEC-2001.
XX
PF 13-JUN-2001; 2001MO-0519178.
XX
PR 16-JUN-2000; 2000US-212336P.
PR 22-JUN-2000; 2000US-213955P.
PR 29-JUN-2000; 2000US-215336P.
PR 07-JUL-2000; 2000US-216821P.
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PR 14-JUL-2000; 2000US-218946P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Elliott VS, Gandhi AR, Lal P, Au-young J, Tribouley CM;
PI Deleage AM, Baughn MR, Nguyen DB, Lee EA, Hatella A, Khan FA;
PI Walla NK, Yao MG, Lu DM, Patterson C, Tang YT, Walsh RT;
PI Azimzai Y, Lu Y, Rankumar J, Xu Y, Reddy R, Das D, Kearney L;
PI Kallick DA;
DR WPI; 2002:090437/12.
DR N-PSDB; ABK12892.
XX
PT Twenty one human proteases (referred to as PR7S-1 to PR7S-21), useful
PT in the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), cardiovascular (e.g. atherosclerosis) and cell
PT proliferative (e.g. cancer) disorders.
XX
PS Claim 1; Page 140-142; 177pp; English.
XX
CC The present invention relates to twenty one new human proteases,
CC referred to as PR7S-1 to PR7S-21. The PR7S polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal e.g. gastritis, esophageal carcinoma and
CC Crohn's disease, cardiovascular e.g. atherosclerosis, hypertension and
CC myocardial infarction, autoimmune/inflammatory e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies and osteoarthritis, cell
CC proliferative e.g. cancer, developmental e.g. Duchenne and Becker
CC muscular dystrophy, epithelial e.g. dermatitis, neurological e.g.
CC epilepsy and Alzheimer's disease and reproductive e.g. infertility and
CC endometriosis disorders. Numerous other examples of each disorder are
CC given in the specification. The present protein sequence represents
CC the human protease PR7S-9 protein of the invention.
XX
SQ Sequence 882 AA;
Query Match 100.0%; Score 4700; DB 23; Length 882;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAMETEOIGVEFEFADCEENESODRKLPEFYERYSMOQLKLLADTRKYHYGM 60
Db 1 MAAMETEOIGVEFEFADCEENESODRKLPEFYERYSMOQLKLLADTRKYHYGM 60
QY 61 AKAPHDFMFKRNDPDSGPHSDRIYLLAMSGENRENTLFYEIPIKTINRAAVLMSKPL 120
Db 61 AKAPHDFMFKRNDPDSGPHSDRIYLLAMSGENRENTLFYEIPIKTINRAAVLMSKPL 120
QY 121 DLFOATLDYGMYSREBELLBERRKIGTVGIASYDYHOGSGTFLEQAGSGIYHKKDGPQG 180
Db 121 DLFOATLDYGMYSREBELLBERRKIGTVGIASYDYHOGSGTFLEQAGSGIYHKKDGPQG 180
QY 181 FTQOPLRPNLVETSCPINRMDPKCPADPDWIAFIHNDIWSINIVREERRLLTYVNEL 240
Db 181 FTQOPLRPNLVETSCPINRMDPKCPADPDWIAFIHNDIWSINIVREERRLLTYVNEL 240
QY 241 ANNEEDARSAGVATFVLOEEFDRSGYWCMPKATETPSGKILRLILEENDESEVEIHH 300
Db 241 ANNEEDARSAGVATFVLOEEFDRSGYWCMPKATETPSGKILRLILEENDESEVEIHH 300
QY 301 TSPMLETRRADSPFRYPKGTANPKVTFKMSIIMDAGRIIIVDKLQPFELFEGVE 360
Db 301 TSPMLETRRADSPFRYPKGTANPKVTFKMSIIMDAGRIIIVDKLQPFELFEGVE 360
QY 361 YIARAGTPEGKYAMSIILDRSOTRLOIVLISPELFPVEDDWERORLIESVDSYTPL 420
Db 361 YIARAGTPEGKYAMSIILDRSOTRLOIVLISPELFPVEDDWERORLIESVDSYTPL 420
QY 421 IYEEETDWINIHDIHFVFPQSHHEEIEFIFASECTGRHLKITSILKESYKRSSG 480
Db 421 IYEEETDWINIHDIHFVFPQSHHEEIEFIFASECTGRHLKITSILKESYKRSSG 480
QY 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNIQVDEVRLVYFEGTKDSPLEHHLVVS 540
Db 481 GLPAPSDFKCPIKEELAITSGEWEVLGRHGSNIQVDEVRLVYFEGTKDSPLEHHLVVS 540
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|||||
Db 481 GLPAPSDFKCPKEIAITSGEMEVLRHGSNIQVDEVRRLVYEGTKDPLEHLLYVS 540
QY 541 YVNGEYTRLDRGYSCHSCISQHCDFEISYSNQNPHCVSLKLSPEDDPTCKTEF 600
Db 541 YVNGEYTRLDRGYSCHSCISQHCDFEISYSNQNPHCVSLKLSPEDDPTCKTEF 600
QY 601 WATILDSAGPLPDYTPPEIFSESTGTGTLXGMLYKPHDLQPKKYPVLFYIGGPVOL 660
Db 601 WATILDSAGPLPDYTPPEIFSESTGTGTLXGMLYKPHDLQPKKYPVLFYIGGPVOL 660
QY 661 VNNRFKGVKFRMLTSLASGLVYVVVINDRSGCHGLKFEKAFKKMQOIEIDDOVEGLQY 720
Db 661 VNNRFKGVKFRMLTSLASGLVYVVVINDRSGCHGLKFEKAFKKMQOIEIDDOVEGLQY 720
QY 721 LASRYDFIDLRVGIHGSYGGYLSLMAQMORSDFRVAIAGAVTLMIIFYDTGYTERYM 780
Db 721 LASRYDFIDLRVGIHGSYGGYLSLMAQMORSDFRVAIAGAVTLMIIFYDTGYTERYM 780
QY 781 GHDPQNGGYVLSGVSAMQAEKFPSEPNRLLLHGFLENVFAHTSILSLFVRAKRPYD 840
Db 781 GHDPQNGGYVLSGVSAMQAEKFPSEPNRLLLHGFLENVFAHTSILSLFVRAKRPYD 840
QY 841 LQIYPOERHSIRVPESEGEHELHLHLQENLGSRIALAKVI 882
Db 841 LQIYPOERHSIRVPESEGEHELHLHLQENLGSRIALAKVI 882

RESULT 5
AAG78415
ID AAG78415 standard; Protein: 882 AA.

XX AAG78415:

DT 12-Apr-2002 (first entry)

De Amino acid sequence of 21953 human prolyl oligopeptidase.

XX 21953 prolyl oligopeptidase; antibody; proline; endopeptidase;
KM cancer; cardiovascular disease; autoimmune disease; atopic allergy;
KM neuronal disorder; vascular disorder; prostate disorder; cytostatic;
KM antidiabetic; antiarthritic; antiasthmatic; antiinflammatory;
KM diabetes mellitus; arthritis; multiple sclerosis; asthma;
KM Grave's disease; neuronal disorder; demyelinating disease.

XX Homo sapiens.

XX MO200179473-A2.

XX 25-OCT-2001.

XX 11-APR-2001; 2001MO-US40483.

XX 18-APR-2000; 2000US-197508P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Meyers RA, Williamson M;

XX WPI: 2002-034353/04.

XX N-PSDB; AAH99934.

XX New polypeptides 21953, member of human prolyl oligopeptidase family,
PT useful as diagnostic targets and therapeutic agents for controlling
XX cancer, lymphoma and leukemia -

XX Claim 1; Page 102-103; 121pp; English.

XX This invention relates to an isolated 21953 human prolyl
CC oligopeptidase. Which is cytostatic, antidiabetic, antiarthritic,
CC neuroprotective, antithyroid, dermatological, antiproliferative,
CC antiasthmatic, ophthalmological, antiinflammatory, nootropic,
CC antiparkinsonian, anticonvulsant, gynecological, vasotropic,

CC antiangiinal, cardiant, antiatherosclerotic, anorectic and
CC metabolic in its action. Uses include gene therapy, expression or
CC activity of 21953 protein modulator. It is useful for identifying a
CC compound which binds to it and can be used in preventing, treating
CC or detecting a cellular proliferative or differentiative disorder.
CC The 21953 molecules can act as novel diagnostic targets and therapeutic
CC agents for controlling disorders associated with the aberrant activity
CC or degradation of peptide hormones e.g., disorders associated with cell
CC differentiation and proliferation such as cancer, immune function,
CC reproductive, neurological and cardiovascular function. The 21953
CC molecules are thus useful for treating and preventing cellular
CC proliferative and differentiative disorders, haematopoietic neoplastic
CC disorders, immune disorders such as autoimmune diseases, diabetes
CC mellitus, arthritis, multiple sclerosis, asthma, Grave's disease,
CC neuronal disorders, demyelinating diseases, vascular disorders and
CC metabolism or pain disorders. This sequence represents the amino
CC acid sequence of 21953 human prolyl oligopeptidase.

SQ Sequence 882 AA;

Query Match 100.0%; Score 4700; DB 23; Length 882;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 882; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMETQGLGVEIFETADCEENTESODRPLKEPFYERYYSMSOLKLLADTRKYGGM 60
Db 1 MAAMETQGLGVEIFETADCEENTESODRPLKEPFYERYYSMSOLKLLADTRKYGGM 60
QY 61 AKAPHDFEYKRNPDGHSRITYYLANSGENRENTLFSEIPTINRAAVLMSKPL 120
Db 61 AKAPHDFEYKRNPDGHSRITYYLANSGENRENTLFSEIPTINRAAVLMSKPL 120
QY 121 DLFQATLDYGMYSREBELREKRRTIGVGIASYDYHOGSGFELFOAGSGIYHVADGGPOG 180
Db 121 DLFQATLDYGMYSREBELREKRRTIGVGIASYDYHOGSGFELFOAGSGIYHVADGGPOG 180
QY 181 FTQOPLRNLVETSCPNIRMDPKLCPADPDWIAEIHNSNDIWSNIIVREERLTVHNEL 240
Db 181 FTQOPLRNLVETSCPNIRMDPKLCPADPDWIAEIHNSNDIWSNIIVREERLTVHNEL 240
QY 241 ANMEDARSAGVAFVLOEEDRISGYWCKAETTSRGGKILKILVEENDESEVEIIV 300
Db 241 ANMEDARSAGVAFVLOEEDRISGYWCKAETTSRGGKILKILVEENDESEVEIIV 300
QY 301 TSPMLFTRRADSPRYPKGTANPKVTFKMSIMIDAEGRITDVIDKELIOPEELLFEGVE 360
Db 301 TSPMLFTRRADSPRYPKGTANPKVTFKMSIMIDAEGRITDVIDKELIOPEELLFEGVE 360
QY 361 YIARAGMTPECKYVMSILDRSOTRLOIVLISPELFIPEDDVMEORLIESVPDSVPL 420
Db 361 YIARAGMTPECKYVMSILDRSOTRLOIVLISPELFIPEDDVMEORLIESVPDSVPL 420
QY 421 IYEEETDIWINIHDIHVPOSHBEIEEPIFASECKTGFRHLKYTISLSESKYKSSG 480
Db 421 IYEEETDIWINIHDIHVPOSHBEIEEPIFASECKTGFRHLKYTISLSESKYKSSG 480
QY 481 GLPAPSDFKCPKEIAITSGEMEVLRHGSNIQVDEVRRLVYEGTKDPLEHLLYVS 540
Db 481 GLPAPSDFKCPKEIAITSGEMEVLRHGSNIQVDEVRRLVYEGTKDPLEHLLYVS 540
QY 541 YVNGEYTRLDRGYSCHSCISQHCDFEISYSNQNPHCVSLKLSPEDDPTCKTEF 600
Db 541 YVNGEYTRLDRGYSCHSCISQHCDFEISYSNQNPHCVSLKLSPEDDPTCKTEF 600
QY 601 WATILDSAGPLPDYTPPEIFSESTGTGTLXGMLYKPHDLQPKKYPVLFYIGGPVOL 660
Db 601 WATILDSAGPLPDYTPPEIFSESTGTGTLXGMLYKPHDLQPKKYPVLFYIGGPVOL 660
QY 661 VNNRFKGVKFRMLTSLASGLVYVVVINDRSGCHGLKFEKAFKKMQOIEIDDOVEGLQY 720
Db 661 VNNRFKGVKFRMLTSLASGLVYVVVINDRSGCHGLKFEKAFKKMQOIEIDDOVEGLQY 720
QY 721 LASRYDFIDLRVGIHGSYGGYLSLMAQMORSDFRVAIAGAVTLMIIFYDTGYTERYM 780

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Db 721 LASRYDFIDLRVGIHGSYGYLSLMLMQRSDIFRYAIGAPVTLMIFYDTGYTERYM 780
QY 781 GHPDQNEGYLLGSVAMQAEKFPSEPNRLLLHGFLEDNVHFARTSILLSLVRAKGRYD 840
Db 781 GHPDQNEGYLLGSVAMQAEKFPSEPNRLLLHGFLEDNVHFARTSILLSLVRAKGRYD 840
QY 841 LQIYPOERHSIRVPESGEHYELHLHYLOENLGSRIALAKYI 882
Db 841 LQIYPOERHSIRVPESGEHYELHLHYLOENLGSRIALAKYI 882

RESULT 6
ABR97361
ID ABR97361 standard; Protein: 782 AA.
XX
AC ABR97361;
XX
DT 27-JUN-2002 (first entry)
XX
DE Novel human protein SEQ ID NO: 629.
XX
KW Human; anti-naemic; vulnerary; anti-inflammatory; immunomodulator;
KW anti-infectivity; cerebroprotective; cytosolic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
XX
XX expressed sequence tag.
XX
OS Homo sapiens.
XX
PN W0200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001MO-US26015.
XX
PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI: 2002-292408/33.
DR N-PSDB: ABN32547.
XX
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Example 2; SEQ ID NO 629; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention.
XX
SQ Sequence 782 AA;

Query Match 87.6%; Score 4118; DB 23; Length 782;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 782; Conservative 0; Mismatches 0; Indels 100; Gaps 1;

QY 1 MAAMETEQLEVEIFETADCEENIESODRPLKEPFYVRYMSQLKLADTRKHGYMM 60
Db 1 MAAMETEQLEVEIFETADCEENIESODRPLKEPFYVRYMSQLKLADTRKHGYMM 60
QY 61 AKAPHDEFVARNPDGPHSDRIYYLAMSNGENRENTLFYSEIPKTIINRAAVLMLSWKPL 120
Db 61 AKAPHDEFVARNPDGPHSDRIYYLAMSNGENRENTLFYSEIPKTIINRAAVLMLSWKPL 120

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Db 61 AKAPHDEFVARNPDGPHSDRIYYLAMSNGENRENTLFYSEIPKTIINRAAVLMLSWKPL 120
QY 121 DLFOATLDYGMYSREELERKRRTGTVGASXYHOGSGFLEQASGIYHVGDGPOG 180
Db 121 DLFOATLDYGMYSREELERKRRTGTVGASXYHOGSGFLEQASGIYHVGDGPOG 180
QY 181 FTQOPLRPNLVEITSCPNIRMDPKLCPADPDWIAEIHNSNDIWSINIYREERRLTYVHNE 240
Db 181 FTQOPLRPNLVEITSCPNIRMDPKLCPADPDWIAEIHNSNDIWSINIYREERRLTYVHNE 240
QY 241 ANMEDARSAGVATFVLOEEDFRTSGYWCCKAETTSGGKILALILENDESEVEIITHV 300
Db 241 ANMEDARSAGVATFVLOEEDFRTSGYWCCKAETTSGGKILALILENDESEVEIITHV 300
QY 301 TSPMLETRRADSPFRPKGTANPKVTFPMSEIMIDAEGRIIDVIDKELIOFELLFEGVE 360
Db 301 TSPMLETRRADSPFRPKGTANPKVTFPMSEIMIDAEGRIIDVIDKELIOFELLFEGVE 360
QY 361 YIARAGWTPCKGVAMSILLDRSQTRLQIVLISPFLFIPVEDDVNERORLIESVDSVYPL 420
Db 361 YIARAGWTPCKGVAMSILLDRSQTRLQIVLISPFLFIPVEDDVNERORLIESVDSVYPL 420
QY 421 IYEEETDIWINIHDIRVFPQSHHEEIEFTFASBCKTGFMHLKITSILKESYKRS 480
Db 421 IYEEETDIWINIHDIRVFPQSHHEEIEFTFASBCKTGFMHLKITSILKESYKRS 480
QY 481 GLPAPSDPKCPKEIATTSGEWEVLGRHGSNIQVDEYRRLVYFEGTKDPSLEHHLVYS 540
Db 481 GLPAPSDPKCPKEIATTSGEWEVLGRHGSNIQVDEYRRLVYFEGTKDPSLEHHLVYS 540
QY 541 YVNPGEVTRLTDGYSHSCISQHCDFEISYKSNQKNHCVSLKLSPEDDPTCKTKEF 600
Db 541 YVNPGEVTRLTDGYSHSCISQHCDFEISYKSNQKNHCVSLKLSPEDDPTCKTKEF 600
QY 601 WATLIDSAGPLPDYTPPEIFSESTGTGLYGMLYKPHDLQPKKYPVLFYIGPOVOL 660
Db 601 WATLIDSAGPLPDYTPPEIFSESTGTGLYGMLYKPHDLQPKKYPVLFYIGPOVOL 660
QY 661 VNNRFKGVKYFRMLNTLASLGVVVVIDNRGSHGKLFKGAFFKMQGLEIDQVEGLQY 720
Db 661 VNNRFKGVKYFRMLNTLASLGVVVVIDNRGSHGKLFKGAFFKMQGLEIDQVEGLQY 720
QY 721 LASRYDFIDLRVGIHGSYGYLSLMLMQRSDIFRYAIGAPVTLMIFYDTGYTERYM 780
Db 721 LASRYDFIDLRVGIHGSYGYLSLMLMQRSDIFRYAIGAPVTLMIFYDTGYTERYM 780
QY 781 GHPDQNEGYLLGSVAMQAEKFPSEPNRLLLHGFLEDNVHFARTSILLSLVRAKGRYD 840
Db 781 GHPDQNEGYLLGSVAMQAEKFPSEPNRLLLHGFLEDNVHFARTSILLSLVRAKGRYD 840
QY 841 LQIYPOERHSIRVPESGEHYELHLHYLOENLGSRIALAKYI 882
Db 841 LQIYPOERHSIRVPESGEHYELHLHYLOENLGSRIALAKYI 882

RESULT 7
ABR97362
ID ABR97362 standard; Protein: 724 AA.
XX
AC ABR97362;
XX
DT 27-JUN-2002 (first entry)
XX
DE Novel human protein SEQ ID NO: 630.
XX
KW Human; anti-naemic; vulnerary; anti-inflammatory; immunomodulator;
KW anti-infectivity; cerebroprotective; cytosolic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
XX
XX expressed sequence tag.
XX
OS Homo sapiens.
XX
PN W0200222660-A2.

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XX 21-MAR-2002.
PD 10-SEP-2001; 2001MO-US26015.
XX 11-SEP-2000; 2000US-0659671.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX MPI: 2002-292408/33.
DR N-PSDB; ABR32548.
XX An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX Example 2; SEQ ID NO 630; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention.
XX
XX Sequence 724 AA:
SQ
Query Match 80.2%; Score 3771; DB 23; Length 724;
Best Local Similarity 82.1%; Pred. No. 0;
Matches 724; Conservative 0; Mismatches 0; Indels 158; Gaps 2;
QY 1 MAAMETEQLGVEIFETADCEENIESODRKLPEFYERYSWSQLKLLADTRKYHYGM 60
DB 1 MAAMETEQLGVEIFETADCEENIESODRKLPEFYERYSWSQLKLLADTRKYHYGM 60
QY 61 AKAPHEMFYKRNDRPGRHSDRIYLLAMSGENRENTLFYSEIKRTIRAVLMSKPL 120
DB 61 AKAPHEMFYKRNDRPGRHSDRIYLLAMSGENRENTLFYSEIKRTIRAVLMSKPL 120
QY 121 DLFQATLDYGMYSREELLERKRRTGIVGASYDHQSGTFLQAGSGIYHVKDGGPG 180
DB 121 DLFQ----- 124
QY 181 FTQQLRPNLVETSCPNIRMDPKLCPADPMIAFIHNSDIWISNIVTREBRRLTYVHNL 240
DB 125 --QQPLRPNLVETSCPNIRMDPKLCPADPMIAFIHNSDIWISNIVTREBRRLTYVHNL 182
QY 241 ANNEEDARSAGVATFVLQEEFDYSGYWCMPKATTPSGKILRLILEENDESEVELIH 300
DB 183 ANNEEDARSAGVATFVLQEEFDYSGYWCMPKATTPSGKILRLILEENDESEVELIH 242
QY 301 TSPMLETRADSRFRYKGTGANKVTFKMSIMIDAGRIIDVYDKLIOPFELFGVE 360
DB 243 TSPMLETRADSRFRYKGTGANKVTFKMSIMIDAGRIIDVYDKLIOPFELFGVE 302
QY 361 YIYRAGTPEGKAWMSILLDRSOTRLQIVLISPELFIPVEDDWERQRLIESVDSVTP 420
DB 303 YIYRAGTPEGKAWMSILLDRSOTRLQIVLISPELFIPVEDDWERQRLIESVDSVTP 362
QY 421 IITEETDIIINHDIFHVPQSHHEIEIFASECTGGRHLKITSILKESKYKSSG 480
DB 363 IITEETDIIINHDIFHVPQSHHEIEIFASECTGGRHLKITSILKESKYKSSG 422
QY 481 GLPAPDSFKPIKEELAITSGEWEVLGRHGSNIQVDEVRRLYFEETKDSPLEHHLTV 540
DB 423 GLPAPDSFKPIKEELAITSGEWEVLGRHGSNIQVDEVRRLYFEETKDSPLEHHLTV 482

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QY 541 YVNPGEVTRLDRGYSHCSCISQHCDFISKYSNOKNPHCVSLYKLSPEDDPTCKTKEP 600
DB 483 YVNPGEVTRLDRGYSHCSCISQHCDFISKYSNOKNPHCVSLYKLSPEDDPTCKTKEP 542
QY 601 WATILDSAGFLPDYTPPEIFSFESTGTFTLYGMLYKPHDIQPGKPYTVLFIYGGPOVOL 660
DB 543 WATILDSAGFLPDYTPPEIFSFESTGTFTLYGMLYKPHDIQPGKPYTVLFIYGGPO --- 599
QY 661 VNNRFGVKYFRLMTLASLQYVVVVIDNRGSCRHGLKFEGAFPKYKMGQIEIDQVEQLQY 720
DB 600 ----- 599
QY 721 LASHYDFIDLRVGHGWSYGYLSLMAQMQRSDIFRVAAGAPVTLMFYDTGYTERYM 780
DB 600 ----- VALAGAPVTLMFYDTGYTERYM 622
QY 781 GHPDNEQGYLGSVAMQAEKFPSEPRKLLHGFIDENVHFATSTILSLFVRAKPYD 840
DB 623 GHPDNEQGYLGSVAMQAEKFPSEPRKLLHGFIDENVHFATSTILSLFVRAKPYD 682
QY 841 LQIYPOERHSIRPESGEHELMHLHYLOENLGRIALKVI 882
DB 683 LQIYPOERHSIRPESGEHELMHLHYLOENLGRIALKVI 724
RESULT 8
ABG61600
ID ABG61600 standard; Protein; 658 AA.
XX
XX ABG61600;
XX
XX 12-AUG-2002 (first entry)
XX
XX Human DPPP-1 splice variant #7.
XX
XX Human: serine protease; dipeptidyl peptidase IV-related protein; DPPP;
XX DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
XX diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
XX heart failure; hypertension; urinary retention; osteoporosis; cancer;
XX ulcer; allergy; cancer; psychotic disorder; neurological disorder;
XX dyskinesia; reproductive disorder; inflammatory disorder;
XX metabolic disorder.
XX
XX Homo sapiens.
XX
XX WO200231134-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001MO-US31874.
XX
XX 12-OCT-2000; 2000US-240117P.
XX
XX (FERR) FERRING BV.
XX
XX Qi S, Akinsanya KO, Riviere PJ, Junien J;
XX MPI: 2002-444178/47.
XX N-PSDB; ABR3331.
XX
XX New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
XX the proteins, useful for treating e.g. fungal, bacterial, protozoan and
XX viral infections, cancers, allergies, neurological disorders, or pain
XX
XX Disclosure: Page 70-72; 113pp; English.
XX
XX The present invention relates to the isolation of novel human serine
XX proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
XX CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
XX and nucleic acids encoding them are useful for treating infections
XX such as fungal, bacterial, protozoan and viral infections, particularly
XX infections caused by human immunodeficiency virus (HIV-1 or HIV-2),

```

CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.

XX
 XX Sequence 658 AA:

Query Match 74.6%; Score 3504; DB 23; Length 658;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MAAMETEOGLVEFEFADCEENIESODRPLEFVYERYSMSOLKLLADTRKHGYMM 60
 DB 1 MAAMETEOGLVEFEFADCEENIESODRPLEFVYERYSMSOLKLLADTRKHGYMM 60
 QY 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBNRENTLFYSEIKPTIRAAVLMLSMKPPL 120
 DB 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBNRENTLFYSEIKPTIRAAVLMLSMKPPL 120
 QY 121 DLFOATLDYGMYSREBELLRERKRIGVGLASYDYHOGSGTFLEQAGSGIYHVADGPG 180
 DB 121 DLFOATLDYGMYSREBELLRERKRIGVGLASYDYHOGSGTFLEQAGSGIYHVADGPG 180
 QY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDMIAFIHSDNIMISNIVREERRLYYVNNEL 240
 DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDMIAFIHSDNIMISNIVREERRLYYVNNEL 240
 QY 241 ANMEDARSAGVATFVLOEEDRYSGYWCPCAKETTPSGKILRILEYEENDESEVEIHH 300
 DB 241 ANMEDARSAGVATFVLOEEDRYSGYWCPCAKETTPSGKILRILEYEENDESEVEIHH 300
 QY 301 TSPMLERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIOFELLFEGVE 360
 DB 301 TSPMLERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIOFELLFEGVE 360
 QY 361 YIARAGTPEKRYAMSLILDSQTRLOIVLSPFLFIPVEDVNERORLISSVDSVTPL 420
 DB 361 YIARAGTPEKRYAMSLILDSQTRLOIVLSPFLFIPVEDVNERORLISSVDSVTPL 420
 QY 421 IYETTDIWINIHIDIFHVPQSHHEEIEFISECKTGFRLHLYKTSILKESKYKSSG 480
 DB 421 IYETTDIWINIHIDIFHVPQSHHEEIEFISECKTGFRLHLYKTSILKESKYKSSG 480
 QY 481 GLPAPSFQKCIKEIATITSGEMVILGRHGSNIQVDEVRRILVYEGTRDSPLEHLLYVVS 540
 DB 481 GLPAPSFQKCIKEIATITSGEMVILGRHGSNIQVDEVRRILVYEGTRDSPLEHLLYVVS 540
 QY 541 YVNGEYTRLDGRYSHSCCISQHCDEFISKYSNOKNPHCVSLKLSPEDDPCKTKEF 600
 DB 541 YVNGEYTRLDGRYSHSCCISQHCDEFISKYSNOKNPHCVSLKLSPEDDPCKTKEF 600
 QY 601 WATILDSAGLPDYTPPEIFESFESTGTGLYGLMKRPHDLPGRKKYPTVLEFYGG 655
 DB 601 WATILDSAGLPDYTPPEIFESFESTGTGLYGLMKRPHDLPGRKKYPTVLEFYGG 655

RESULT 9

ABG61596 ID ABG61596 standard; Protein; 661 AA.

XX AC ABG61596;

XX DT 12-AUG-2002 (first entry)

XX DE Human DPRP-1 splice variant #3.

XX Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;

KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.

XX Homo sapiens.

XX PN W0200231134-A2.

XX PD 18-APR-2002.

XX PF 12-OCT-2001; 2001WO-US31874.

XX PR 12-OCT-2000; 2000US-240117P.

XX PA (FERR) FERRING BV.

XX PI Q1 S, Akinsanya KO, Riviere PJ, Junien J;

XX DR WPI; 2002-444178/47.

XX DR N-PSDB; ABK83327.

PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain

XX

XX PS Disclosure; Page 63-65; 113pp; English.

XX CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)

CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly

CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,

CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,

CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or

CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and

CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.

CC XX Sequence 661 AA:

Query Match 74.6%; Score 3504; DB 23; Length 661;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAMETEOGLVEFEFADCEENIESODRPLEFVYERYSMSOLKLLADTRKHGYMM 60
 DB 1 MAAMETEOGLVEFEFADCEENIESODRPLEFVYERYSMSOLKLLADTRKHGYMM 60
 QY 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBNRENTLFYSEIKPTIRAAVLMLSMKPPL 120
 DB 61 AKAPHDFMEYKRNDDGPHSDRIYYLAMSGBNRENTLFYSEIKPTIRAAVLMLSMKPPL 120
 QY 121 DLFOATLDYGMYSREBELLRERKRIGVGLASYDYHOGSGTFLEQAGSGIYHVADGPG 180
 DB 121 DLFOATLDYGMYSREBELLRERKRIGVGLASYDYHOGSGTFLEQAGSGIYHVADGPG 180
 QY 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDMIAFIHSDNIMISNIVREERRLYYVNNEL 240
 DB 181 FTQOPLRPNLVETSCPNIRMDPKLCPADPDMIAFIHSDNIMISNIVREERRLYYVNNEL 240
 QY 241 ANMEDARSAGVATFVLOEEDRYSGYWCPCAKETTPSGKILRILEYEENDESEVEIHH 300
 DB 241 ANMEDARSAGVATFVLOEEDRYSGYWCPCAKETTPSGKILRILEYEENDESEVEIHH 300
 QY 301 TSPMLERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIOFELLFEGVE 360
 DB 301 TSPMLERRADSFYRPTGTANPKVTFKMSIIMDAGRIIDVIDKELIOFELLFEGVE 360

OY 361 YIARAGWTPGKYAMSIILDRSQTRLQIVLISPELFIPEDDVNERORLIESVDSVTPPL 420
 DB 361 YIARAGWTPGKYAMSIILDRSQTRLQIVLISPELFIPEDDVNERORLIESVDSVTPPL 420
 OY 421 IYIETTDIWINHIDIRVFPQSHSEELIEFIASECKTGRHLKYITSLIKESKRRSSG 480
 DB 421 IYIETTDIWINHIDIRVFPQSHSEELIEFIASECKTGRHLKYITSLIKESKRRSSG 480
 OY 481 GLPAPSDFKCPKEIEIATTSGEVNLGRHGSNIQVDEVRLVYEGTKDSPLEHHLVVS 540
 DB 481 GLPAPSDFKCPKEIEIATTSGEVNLGRHGSNIQVDEVRLVYEGTKDSPLEHHLVVS 540
 OY 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQKNPHCVSLYKLSPEDDPTCKTKEF 600
 DB 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQKNPHCVSLYKLSPEDDPTCKTKEF 600
 OY 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLPGRKKYPTVLFYIGG 655
 DB 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLPGRKKYPTVLFYIGG 655

RESULT 10

ABG61594 standard; Protein: 690 AA.

ID ABG61594

AC ABG61594:

DT 12-AUG-2002 (first entry)

DE Human DPPR-1 splice variant #1.

XX Human; serine protease; dipeptidyl peptidase IV-related protein; DPPR;

XX DPPR; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;

XX diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;

XX heart failure; hypertension; urinary retention; osteoporosis; cancer;

XX ulcer; allergy; cancer; psychotic disorder; neurological disorder;

XX dyslexia; reproductive disorder; inflammatory disorder;

XX metabolic disorder.

OS Homo sapiens.

XX Homo sapiens.

XX WO200231134-A2.

XX 18-APR-2002.

XX 12-OCT-2001: 2001MO-US31874.

XX 12-OCT-2000: 2000US-240117P.

XX (FERR) FERRING BV.

XX Q1 S, Akimsanya KO, Riviere PJ, Junien J;

XX WPI; 2002-444178/47.

XX N-PSDB; ABK83325.

XX New dipeptidyl peptidase IV-related proteins and nucleic acids encoding

XX the proteins, useful for treating e.g. fungal, bacterial, protozoan and

XX viral infections, cancers, allergies, neurological disorders, or pain

XX Disclosure: Page 59-61; 113pp: English.

XX The present invention relates to the isolation of novel human serine

XX proteases referred to as dipeptidyl peptidase IV (DPPIV)-related

XX proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)

XX and nucleic acids encoding them are useful for treating infections

XX such as fungal, bacterial, protozoan and viral infections, particularly

XX infections caused by human immunodeficiency virus (HIV-1 or HIV-2),

XX pain, diabetes, precocious puberty, infertility, obesity, anorexia,

XX bullma, Parkinson's disease, acute heart failure, hypotension,

XX hypertension, urinary retention, osteoporosis, angina pectoris,

CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPPR proteins.

SQ Sequence 690 AA;

Query Match 74.6%; Score 3504; DB 23; Length 690;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 655; Conservative 0; Indels 0; Gaps 0;

Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAMETEOGLVEIETADCEENIESQDRPKLEPPYVERYSWSQKLLADTRKRYHGM 60

DB 1 MAAMETEOGLVEIETADCEENIESQDRPKLEPPYVERYSWSQKLLADTRKRYHGM 60

OY 61 AKAPHDMEFVKRNDPDGSHSDRIYLLAMSGENRNTLFYSEIPTINRAVLAWSMPL 120

DB 61 AKAPHDMEFVKRNDPDGSHSDRIYLLAMSGENRNTLFYSEIPTINRAVLAWSMPL 120

OY 121 DLFOATLDYGYSRREELLREKRIGTVGIASYDYHQSGLFLOAGSGIYHVKDGPQG 180

DB 121 DLFOATLDYGYSRREELLREKRIGTVGIASYDYHQSGLFLOAGSGIYHVKDGPQG 180

OY 181 FTQOPLRNLVETSCPNIRMDPKLCPADPDWIAFTHSNDIMISNIVTREBRRLTYVHNL 240

DB 181 FTQOPLRNLVETSCPNIRMDPKLCPADPDWIAFTHSNDIMISNIVTREBRRLTYVHNL 240

OY 241 ANMEDARSAGVATFVLOEEDRISGYWMCRAETTPSGGKILKILENDESEYEIIV 300

DB 241 ANMEDARSAGVATFVLOEEDRISGYWMCRAETTPSGGKILKILENDESEYEIIV 300

OY 301 TSPMLERARAFYRPTGTANPKVTFKMSIMIDAERIIDVIDKELIOFELLFEGVE 360

DB 301 TSPMLERARAFYRPTGTANPKVTFKMSIMIDAERIIDVIDKELIOFELLFEGVE 360

OY 361 YIARAGWTPGKYAMSIILDRSQTRLQIVLISPELFIPEDDVNERORLIESVDSVTPPL 420

DB 361 YIARAGWTPGKYAMSIILDRSQTRLQIVLISPELFIPEDDVNERORLIESVDSVTPPL 420

OY 421 IYIETTDIWINHIDIRVFPQSHSEELIEFIASECKTGRHLKYITSLIKESKRRSSG 480

DB 421 IYIETTDIWINHIDIRVFPQSHSEELIEFIASECKTGRHLKYITSLIKESKRRSSG 480

OY 481 GLPAPSDFKCPKEIEIATTSGEVNLGRHGSNIQVDEVRLVYEGTKDSPLEHHLVVS 540

DB 481 GLPAPSDFKCPKEIEIATTSGEVNLGRHGSNIQVDEVRLVYEGTKDSPLEHHLVVS 540

OY 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQKNPHCVSLYKLSPEDDPTCKTKEF 600

DB 541 YVNPGEVTRLDRGYSHSCCISQHCDFEISKYSNQKNPHCVSLYKLSPEDDPTCKTKEF 600

OY 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLPGRKKYPTVLFYIGG 655

DB 601 WATILDSAGPLPDYTPPEIFSFESTTGTLYGMLYKPHDLPGRKKYPTVLFYIGG 655

XX RESULT 11

XX AAB93565

XX ID AAB93565 standard; Protein: 632 AA.

XX AAB93565:

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:12964.

XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EPI074617-A2.

XX

PD 07-FEB-2001.
 XX
 PE 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 12964; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AA892446 to
 CC AA895893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX
 SQ Sequence 632 AA:
 Query Match 70.9%; Score 3333.5; DB 22; Length 632;
 Best Local Similarity 92.4%; Pred. No. 2.3e-312;
 Matches 631; Conservative 0; Mismatches 1; Indels 51; Gaps 1;
 1;
 QY 200 MDPKLCPADPWIAFIHSNDIWSINVTREERLTYVNELANMEDARSGAVTFVLOE 259
 DB 1 MDPKLCPADPWIAFIHSNDIWSINVTREERLTYVNELANMEDARSGAVTFVLOE 60
 QY 260 EFDRTSGYMWCPKATETPSSGKILRLIYEENDESEVELIHTSPMLERRADSEFYPTKG 319
 DB 61 EFDRTSGYMWCPKATETPSSGKILRLIYEENDESEVELIHTSPMLERRADSEFYPTKG 120
 QY 320 TANPKVTFKMEIMIDAGRIIDVYDKELIOPFELIFGEVEYIARAGTPEGKYAMSTLL 379
 DB 121 TANPKVTFKMEIMIDAGRIIDVYDKELIOPFELIFGEVEYIARAGTPEGKYAMSTLL 180
 QY 380 DRSOTRIQIVILSPPLIPVEDDVMERQRLIESVPDSVTPILTYEETDWINIHDFHV 439
 DB 181 DRSOTRIQIVILSPPLIPVEDDVMERQRLIESVPDSVTPILTYEETDWINIHDFHV 240
 QY 440 FPOSHHEETIEFPASECTGFRHLKYITSLIKESKYRSSGGLPAPSPKCPKEEIAIT 499
 DB 241 FPOSHHEETIEFPASECTGFRHLKYITSLIKESKYRSSGGLPAPSPKCPKEEIAIT 300

QY 500 SGEMEVILGRHGSNIQVDEVRRLVVEEGTKDSPLEHHLVVSYNVGEVTRLTDRGYSHC 559
 DB 301 SGEMEVILGRHGSNIQVDEVRRLVVEEGTKDSPLEHHLVVSYNVGEVTRLTDRGYSHC 360
 QY 560 CISOHCDEFISKYSNOKNPHCVSLKLSPPDDPCKTKEWATILDSAGLPDPTPEI 619
 DB 361 CISOHCDEFISKYSNOKNPHCVSLKLSPPDDPCKTKEWATILDSAGLPDPTPEI 420
 QY 620 FSPSTGTFTLYGMKYRPHDLOPGKKYPTVLFYGGPOVOLVNNRFGVKERTLNTLASL 679
 DB 421 FSPSTGTFTLYGMKYRPHDLOPGKKYPTVLFYGGPOVOLVNNRFGVKERTLNTLASL 480
 QY 680 GYVVVVVDNRGSCRGKLFEGAFYKKMGQLEIDDQEGLOYLASRYDFIDDRVGIHGS 739
 DB 481 GYVVVVVDNRGSCRGKLFEGAFYKKMGQLEIDDQEGLOYLASRYDFIDDRVGIHGS 507
 QY 740 YGYLISLMALMQRSDIFPVATAGAPVTLWITYDGYTERVNGHPDQNGYLLCSVMOA 799
 DB 508 -----VAIAGAPVTLWITYDGYTERVNGHPDQNGYLLCSVMOA 549
 QY 800 EKFPSEPNRLLLHGFIDENVHPAHTSTLSLFLVRAGKPYDLOIYPOBRHSIRPESGEH 859
 DB 550 EKFPSEPNRLLLHGFIDENVHPAHTSTLSLFLVRAGKPYDLOIYPOBRHSIRPESGEH 609
 QY 860 YELHLHYLQENLGSRIALAKVI 882
 DB 610 YELHLHYLQENLGSRIALAKVI 632
 RESULT 12
 ID ABG61601 standard; Protein; 613 AA.
 XX
 AC ABG61601;
 XX
 DT 12-AUG-2002 (first entry)
 XX
 DE Human DPRP-1 splice variant #8.
 XX
 KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinnesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 PN M0200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US31874.
 XX
 PR 12-OCT-2000; 2000US-240117P.
 XX
 PA (FERR) FERRING BV.
 XX
 PI Qi S, Akinsanya KO, Riviere PJ, Junien J;
 XX
 DR WPI; 2002-444178/47.
 DR N-PSDB; ABK83332.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 PT
 XX
 PS Disclosure; Page 73-75; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related

QY 334 IDAEGRIIDVIDKELIOPELIFEGVEYIARAGWTPESGKAMSILLDRSOTRLOIVLISP 393
 PT 324 TDSOGKIYSTOKEKELVOPFSSLPFKVEYIARAGWTRDCKYAMAMFLDRPQOMLOLVLLPP 383
 Db 394 ELFIPEVDVNERORLIESVDSVTPPLIYEETDWINIHIDIFHVPOSH-EEIEEIF 452
 XX 384 ALFIPTENEBORLASARAVPRNVPYVVEEVINWVINDIPEFPFSGEDELCELR 443
 QY 453 ASECKTGRHLKYKITSILKESKYSRSGGLPAPSDFCPIKEEIALTSGEVEIGRHNSN 512
 Db 444 ANECKTGRCHLYKVTAVLKSOGYDMSEPFSGEDEFKCPKEEIALTSGEVEIGRHNSK 503
 QY 513 IOVDEVRLLYVEGTSKSPLEHLLVYVSVNPGVTRLTDRGYSHSCCISOCHDFEISKY 572
 Db 504 IWNVEETKLYVEFGTKDPLREHLLVYVSEAAGEIVRLTFGFSHSCSMQNFDMFVSHY 563
 QY 573 SNOKNPHCVSLYKLSSEDDPTCKTEKFWATILDSAGPLPYTPPELFSFESTGTFLYG 632
 Db 564 SSVSTPFCVHYVYKLSGDDPLHKKQPRFWMASMEASCPDPYVPELTFHFTTRSDVRLYG 623
 QY 633 MLYRPHDLOPGKKYPTVLFYIGGPOVOVLNRRFGVKYERLNTLASIGYVVVINDNRSC 692
 Db 624 MLYRPHALOPKKHPTVLFYVGGPOVOLVNSFGIKRLNTLASIGYVVVINDNRSC 683
 QY 693 HRGLKFEAGFYKMGQIEIDDOVEGLQYLASRYDFIDLRVGIHGSYGYLSMALMQR 752
 Db 684 ORGLRFEGLKNGQVIEIDDOVEGLQYVAEKYGFIDLSVAIHGWSYGGFSLMGLIHK 743
 QY 753 SDIRVNAAGAPVTLMTFYOTGTYERKYGHPDNOEGYLCVSAMQAKFSEPERLL 812
 Db 744 PÖVERVALAGAPVTVMAVDTGYERYMDVPENNOHGEAGSVALHVEKLENEPRLLIL 803
 QY 813 HGFIDENVHFHTSILSFLVRAGKPYDLOIYPOERHSIRPESGEHEHLLHLOENL 872
 Db 804 HGFIDENVHFHTFVLSQLIRAKRPYDLOIYPRNHSIRPESGEHEVTLHFLQYL 863
 RESULT 14
 ID ABG61602 standard; Protein: 892 AA.
 XX ABG61602:
 AC ABG61602:
 DT 12-AUG-2002 (first entry)
 XX DE Human DPRP-2 splice variant #1.
 XX KW Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP;
 KW DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinesia; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.
 XX OS Homo sapiens.
 XX PN WO20023134-A2.
 XX PD 18-APR-2002.
 XX PF 12-OCT-2001; 2001MO-US31874.
 XX PR 12-OCT-2000; 2000US-240117P.
 XX PA (FERR) FERRING BV.
 XX Q1 S, Akinsanya KO, Riviere PJ, Junien J;
 XX WPI: 2002-444178/47.
 XX DR N-PSDB; ABR3333.
 XX

PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 XX
 PS Disclosure; Page 76-78; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
 CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinesias. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
 CC
 XX Sequence 892 AA;
 SO
 Query Match 61.1%; Score 2870; DB 23; Length 892;
 Best Local Similarity 61.5%; Pred. No. 2,4e-267;
 Matches 517; Conservative 134; Mismatches 187; Indels 2; Gaps 2;
 QY 35 FVERYSWQKLKLLADPRKHGYMMAKAPHDVFNKNDPDDGSHSRITYLAMSNGRE 94
 Db 53 FOYOKHSDGLRSTIHGSRKYSGLVNAKPAHDFOVOKTDSGSHSLYLGMPYSGRE 112
 QY 95 NTFESELPIKTINRAAVLMLSMKPLDLFOATLDYGMYSREELREKRIGTVGIASYD 154
 Db 113 NSLXSELPKVRKREALLLSMKQMLDHFQATPHHGVYSREELREKRIGTVGINSYD 172
 QY 155 YHGGSGTFLFQAGSGIYHVKDCGPGFTQDPLRNLVETSPNIRMDKLCPADPWIAF 214
 Db 173 FHSSEGLFLFQAGSNLSLFCRBDGKNGFVSPMKPLEIKTQCSPPMDKICPADPAFSE 232
 QY 215 IHSNDIWSNIVTREERLTVVHNELAMMEDASAGATVLOEPPRYSGYWCMPRAE 274
 Db 233 INSDLWANIETGEERLTCHQGLSNVLDPPKASAGATVLOEEDRPFYGMWCPTAS 292
 QY 275 TTPSGG-KILRLIYENDESEVEIHWTSPLERFRADSFYPTGTANPKVTFKMSIEM 333
 Db 293 WESBGLKTLRLIYEVDESEVEIHWTSPLERFRADSFYPTGTANPKVTFKMSIEM 352
 QY 334 IDAEGRIIDVIDKELIOPELIFEGVEYIARAGWTPESGKAMSILLDRSOTRLOIVLISP 393
 Db 353 TDSOGKIYSTOKEKELVOPFSSLPFKVEYIARAGWTRDCKYAMAMFLDRPQOMLOLVLLPP 412
 QY 394 ELFIPEVDVNERORLIESVDSVTPPLIYEETDWINIHIDIFHVPOSH-EEIEEIF 452
 Db 413 ALFIPTENEBORLASARAVPRNVPYVVEEVINWVINDIPEFPFSGEDELCELR 472
 QY 453 ASECKTGRHLKYKITSILKESKYSRSGGLPAPSDFCPIKEEIALTSGEVEIGRHNSN 512
 Db 473 ANECKTGRCHLYKVTAVLKSOGYDMSEPFSGEDEFKCPKEEIALTSGEVEIGRHNSK 532
 QY 513 IOVDEVRLLYVEGTSKSPLEHLLVYVSVNPGVTRLTDRGYSHSCCISOCHDFEISKY 572
 Db 533 IWNVEETKLYVEFGTKDPLREHLLVYVSEAAGEIVRLTFGFSHSCSMQNFDMFVSHY 592
 QY 573 SNOKNPHCVSLYKLSSEDDPTCKTEKFWATILDSAGPLPYTPPELFSFESTGTFLYG 632
 Db 593 SSVSTPFCVHYVYKLSGDDPLHKKQPRFWMASMEASCPDPYVPELTFHFTTRSDVRLYG 652
 QY 633 MLYRPHDLOPGKKYPTVLFYIGGPOVOVLNRRFGVKYERLNTLASIGYVVVINDNRSC 692
 Db 653 MLYRPHALOPKKHPTVLFYVGGPOVOLVNSFGIKRLNTLASIGYVVVINDNRSC 712
 QY 693 HRGLKFEAGFYKMGQIEIDDOVEGLQYLASRYDFIDLRVGIHGSYGYLSMALMQR 752

Db 713 ORGLRFGALKNQMGVEIEDQVEGLQFAEKYGFIDLSRVAIHGWSYGGFLSLMGLINK 772
 QY 753 SDIFRAIAGAVTLMIFFDTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 812
 Db 773 POVFVAIAGAPVTVMAYDTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 832
 QY 813 HGFLEDNVHFAHTSILSLFLVRAGKPYDLOIYPOERHSIRVSGEYELHLHYLOENL 872
 Db 833 HGFLEDNVHFAHTSILSLFLVRAGKPYDLOIYPOERHSIRVSGEYELHLHYLOENL 892

RESULT 15
 ABG61604
 ID ABG61604 standard; Protein: 892 AA.
 AC ABG61604;
 DT 12-AUG-2002 (first entry)
 DE Human DPP-2 splice variant #3.
 XX
 KW Human; serine protease; dipeptidyl peptidase IV-related protein; DPP;
 KW DPP-IV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
 KW diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke;
 KW heart failure; hypertension; urinary retention; osteoporosis; cancer;
 KW ulcer; allergy; cancer; psychotic disorder; neurological disorder;
 KW dyskinetic; reproductive disorder; inflammatory disorder;
 KW metabolic disorder.
 XX
 OS Homo sapiens.
 PN WO200231134-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US31874.
 PR 12-OCT-2000; 2000US-240117P.
 PA (FERR) FERRING BV.
 PI Q1 S, Akinsanya KO, Riviere PJ, Junten J;
 DR WPI: 2002-444178/47.
 DR N-PSDB; ABK83335.
 XX
 PT New dipeptidyl peptidase IV-related proteins and nucleic acids encoding
 PT the proteins, useful for treating e.g. fungal, bacterial, protozoan and
 PT viral infections, cancers, allergies, neurological disorders, or pain
 XX
 PS Disclosure: Page 81-84; 113pp; English.
 XX
 CC The present invention relates to the isolation of novel human serine
 CC proteases referred to as dipeptidyl peptidase IV (DPP-IV)-related
 CC proteins (DPPR). The dipeptidyl peptidase IV-related proteins (DPPR)
 CC and nucleic acids encoding them are useful for treating infections
 CC such as fungal, bacterial, protozoan and viral infections, particularly
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
 CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
 CC psychotic and neurological disorders (e.g. anxiety, dementia, or
 CC schizophrenia), and dyskinetics. These may also be used in discovering
 CC therapeutic agents for the treatment of reproductive, inflammatory and
 CC metabolic disorders. ABG61591-ABG61612 represent human DPP proteins.
 XX
 SQ Sequence 892 AA:

Query Match 61.1%; Score 2870; DB 23; Length 892;
 Best Local Similarity 61.5%; Pred. NO. 2.4e-267;

Matches 517; Conservative 134; Mismatches 187; Indels 2; Gaps 2;
 QY 35 FVYERSYMSQLKLLADTETKYGYMAKAPHDMPKRPNDPGHSRIYLLAMSENE 94
 Db 53 FOYQKSHWDGLSIIHSGSKYSGLLVNAKAPHDFOEQKTDSEGPSHRLYLGMPYSGH 112
 QY 95 NTLFYSIPIKTTINRAVLAWSKPLDLFOATLDGMYGREBELLEERRIGTVGIASVD 154
 Db 113 NSLLYSEIKKVKRKEALLLSKQMDLHFOATPHHGVYSREBELLEERRIGTVGIASVD 172
 QY 155 YHOGSTFLFQAGSGIYHVKDGGPOGFTQPLRPNLVETSCPNIMDPKLCPADPWIAP 214
 Db 173 FHSEGLFLFOASNSLFRHCDGKNGFNWSPMKPLEIKTQSGPMDPKICPADPAFFSF 232
 QY 215 IHSNDIWINIYTRERRLTYVHNELANNEBPASGAVTFVLOEEDFSGVWMPKAE 274
 Db 233 INNSDLWVANIETGEERRLTFCHQGLSNVLDPKSAGVATFVLOEEDFSGVWMPKAE 292
 QY 275 TTPSGGCKILRLILEENDESEVETIHTSPMLETRRADSFYRPAKGTANPKYFKKSEIM 333
 Db 293 WEGSEGLKTLRLILEEVDSEVEVIVHPSPALREKRTDSYRPRGSKPKIALKAEFO 352
 QY 334 IDAEGRIIDVIDKELIQPELLEGEVETARAGWPEGVYAMSILDRSOTRLQIVLISP 393
 Db 353 TDSOCKIVSTOEKELVQPFSSLFPEKVEYIARAGWTRDGVAMAMFLDRPOQWLQVLLP 412
 QY 394 ELFIPEDDVMQRILIESVPSVPLIYEETDWINIHDFHNFPSH-EELEIFTF 452
 Db 413 ALTFPSTENEBORLASARAVPRVQPVYEEVTNIVINHDIETFPQSEGDDELCPKR 472
 QY 453 ASECKTGFPHILYKITSILKESKYKRSSGGLPAPSDKCPKEEIAITSGEWEYVLRHGSN 512
 Db 473 ANECKTGFCHLKVTAVALKSSQGDWSEPPSGDEKCKPIKEEIALTSGEWEYVLRHGSN 532
 QY 513 IOVDYRRLVYFEGTKDSLEHLVYVSVNGEVTRLTRDGYSHSCISQHCDFPISKY 572
 Db 533 IWNNECTKLTYFGCTKDTPEHLVYVSYEAGETIYRLTPGFSHSCSMQNDMFVSHY 592
 QY 573 SNOKNPGVSLYKLSPPEDPTCKTEFNATLIDSGPLPDYTPPTFFSPSTGTGLYG 632
 Db 593 SSVSTPPCYHVYKLSGPDPLHKKORFNAMSEASCPDPYPPETFFHTRSDVRLG 652
 QY 633 MLYRPHDLPGRKKYPTVLEFYGGPOVLVNNRFGKVFRLNTLASLGVVYVINDRGSG 692
 Db 653 MIYKPHALDPGRKKHPTVLEFYGGPOVLVNNRFGKIKYLRNLTASLGAVVYVINDRGSG 712
 QY 693 HNGKFEAGAFKTKMGQIEIDDOVEGLQYLASRTDFIDLRVGIHGSYGGYLSLAMLOR 752
 Db 713 ORGLRFGALKNQMGVEIEDQVEGLQFAEKYGFIDLSRVAIHGWSYGGFLSLMGLINK 772
 QY 753 SDIFRAIAGAPVTLMIFDTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 812
 Db 773 POVFVAIAGAPVTVMAYDTGTERYMGHPPONEGYYLGSVAMQAEKFPSPENRLL 832
 QY 813 HGFLEDNVHFAHTSILSLFLVRAGKPYDLOIYPOERHSIRVSGEYELHLHYLOENL 872
 Db 833 HGFLEDNVHFAHTSILSLFLVRAGKPYDLOIYPOERHSIRVSGEYELHLHYLOENL 892

RESULT 16
 AAE24168
 ID AAE24168 standard; Protein: 969 AA.
 AC AAE24168;
 DT 23-SEP-2002 (first entry)
 DE Human dipeptidyl peptidase 9 (DPP9) protein.
 XX
 KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
 KW autoimmunity; human immunodeficiency virus; HIV infection; cytostatic;
 KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
 KW antiviral; enzyme.

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XX OS Homo sapiens.
XX Key Location/Qualifiers
XX FT Misc-difference 374
XX FT /note= "Encoded by GAA"
XX PN WO200234900-A1.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001: 2001WO-AU01388.
XX PR 27-OCT-2000: 2000AU-0001078.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Abbott CA, Gorrell MD;
XX DR WPI: 2002-454646/48.
XX DR N-PSDB: AAD38954.
XX
XX PT New dipeptidyl peptidase (DPP) peptides, useful for screening
XX PT inhibitors of DPP catalytic activity, which may be employed to treat
XX PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX PT rejection and HIV infection -
XX PS Claim 1: Fig 4; 91pp; English.
XX CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX CC polynucleotides encoding such proteins. The DPP peptides are useful for
XX CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX CC rejection and HIV (human immuno deficiency virus) infection. The present
XX CC sequence is human DPP9 protein.
XX SQ Sequence 969 AA:
XX
XX Query Match 60.9%; Score 2863; DB 23: Length 969;
XX Best local similarity 61.4%; Pred. No. 1.3e-266;
XX Matches 516; Conservative 134; Mismatches 188; Indels 2; Gaps 2;
XX
OY 35 FVYERSMSQKLADTRKRYHGMKAPDHDFMFKRNDPGRPHSDRIYLAAMSGENRE 94
DB 130 FQYQKHSWMDGLRSIIHSGSRKYSGLIVNKAHPDFQVQKTDESGRPHSHRLYLGMPIGSR 189
OY 95 NTFEYGEIPTIRAAVIMSMKRLDLPQATLDYGMYSREELERKRIGVGTASVD 134
DB 190 NSLTYSEIPIKVKKEALDLMSKQMDHFOATPHHGVYSREELLRKRRLGVGGLTSTD 249
OY 155 YHOGSGTFLFOAGSGIYHVKDGGPOGFTQPLRPNLVETSCPNIRMDPKLCPADPMIAF 214
DB 250 FHSSEGLFLFOAGNSLFLHCRDGGKNGFPMSPKPLEIKTQCSGRPMRDKCPADPAFFSF 309
OY 215 IHSNDIWSINIVYREERRLTYHNELANMEDARSAGVATFVLOEEDRYSGYWCCKAE 274
DB 310 NNSMDLVANIEETGEERRLTFCHQGLSNVLDPKSAGVATFVLOEEDRFTGYWCPCPTAS 369
OY 275 TTPSGG-KILRIIYEEDESEVEIIHVTSPMLFTRRSPRYKTPGANKVFFKMSIEM 333
DB 370 WBSGQGLKRLIRIIEYDESEVEYIHPSPALERKIDSTRYRTGSKNKIKALKAEFO 429
OY 334 IDAEGRIIVIDKELIQPEILFEGVEYIARAGWTEGKYAMSILLDRSQTRLQIYLISP 393
DB 430 TDSQGLIVSIOEKELVQPPSLFPRKEYIARAGWTRDGKAYAMFLDRPQOMIQLVLLPP 489
OY 394 ELFIPEEDVMEQRLIESYPSDVTPLIYEETDWINIHDFHVPPOSH-EEIEFTF 452
DB 490 ALFIPESTNEEOGLASARAVPRNVQYVYEEVTNWIMVHDIFYPFPOSEGDECEFLR 549
OY 453 ASCEKGFRLHYKITSLESKYKRSSSGGLPAPSDKCPKEIATISGWEVLGRHGSN 512
DB 550 ANECKGFCFLIKVAVLASQGIWSEPPSPGDEDFRCPIKEIATISGWEVLARHGSK 609

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OY 513 IQYDEVRLVYFEGTCKDSPLEHLLVYVYNBGEVTRLDRGYSHSCCIHQHCFPISKY 572
DB 610 IWNNEETKLIVFGCTKDTPLEHLLVYVYEAAGEIYRLTTPGSHSCSNQNDMEVSHY 669
OY 573 SNQKNCVSLKRLSSPEDDPTCKTEFNATILDSAGLPDITPPIPFSESTGTLYG 632
DB 670 SSVSTPPCVHVVYKLSGPDDDPLHKQPRFMAWMEASCPEDVYPPPIFFHFRSDRLVG 729
OY 633 MLYKPPHLDOPGKKYPTVLFYGGPOVOLVNNRKKGVKRYFLNLTASGLVYVVIDNRGSC 692
DB 730 MLYKPPHLDOPGKKYPTVLFYGGPOVOLVNNRKKGVKRYFLNLTASGLVYVVIDNRGSC 789
OY 693 HRGLKFECAFVKYKMGQIETDDQVEGLQYLASRYDFDLDRVGTHGWSYGYSLMALMOR 752
DB 790 QRLRFEGALKNMGQVEIEDQVEGLQYFAEKYGFIDLSRVATHGWSYGYSLMALMOR 849
OY 753 SDIFRVALGAPVTLWIFDGTTERYMGHPDQNEOGYLYGVAMQAEKFPSPENRLLLL 812
DB 850 PQYKVALIAGAPVTVMVAVDTGYTERYMDVPENNQHGVEAGVVALHVERKLPNEPRLLIL 909
OY 813 HGFLDENVHFAHRSILSLFVLRGKRPYDLOIYPOERHSTIRVPSGHEYLHLHYLOENL 872
DB 910 HGFLDENVHFAHRSILSLFVLRGKRPYDLOIYPOERHSTIRVPSGHEYLHLHYLOENL 969
XX
XX RESULT 17
XX ID AAE24171 standard; Protein: 830 AA.
XX AC AAE24171;
XX XX 23-SEP-2002 (first entry)
XX DT
XX DE Human dipeptidyl peptidase 4 (DPP4)-like 2 protein.
XX KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
XX KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
XX KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
XX KW antiviral; enzyme; DPP-4 like 2 protein.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT Misc-difference 235
XX FT /note= "Encoded by GAG"
XX PN WO200234900-A1.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001: 2001WO-AU01388.
XX PR 27-OCT-2000: 2000AU-0001078.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Abbott CA, Gorrell MD;
XX DR WPI: 2002-454646/48.
XX DR N-PSDB: AAD38957.
XX
XX PT New dipeptidyl peptidase (DPP) peptides, useful for screening
XX PT inhibitors of DPP catalytic activity, which may be employed to treat
XX PT e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX PT rejection and HIV infection -
XX PS Disclosure; Page 82-86; 91pp; English.
XX CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX CC polynucleotides encoding such proteins. The DPP peptides are useful for
XX CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft.

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rejection and HIV (human immuno deficiency virus) infection. The present sequence is human DPP4-like 2 protein.

Sequence 830 AA:

Query Match 60.3%; Score 2835; DB 23; Length 830;

Best Local Similarity 61.7%; Pred. No. 5.2e-264; Matches 512; Conservative 131; Mismatches 185; Indels 2; Gaps 2;

45 LKLLADTRKHYGMMAKAPHDPEFKRNDPDRPHSDRIYLLAMSGENRNTLFYSEIPK 104
 1 LRSIHGSRKRYSGLIYVKAHPDFOVKOTDESGHSHRLYLCPGSRNSLYSEIPK 60
 105 TIRAAVLMISMKPLDLFOATLDYGMYSREELLREKRIGTGVGASDYHOGSGTFLF 164
 61 KVKKEALLLSWKOMLDHQATPHHGYVSREELLREKRRLGVFGITSDVHSESGFLF 120
 165 QAGSGIYHVKDGGPGFTOOLPRNLVETSCPNIRMDPKLCPADPMIAEIHNSDIWISN 224
 121 QASNSLFGHCRDGGKNGFVSPMKPLEIKTCQSGPRMDPKICPADPAFFSPNNNSDLWAN 180
 225 IYTRERRLTYVHNELANMEDARSAGVATFVLOEEFDRISGVWCPKAEITTSOG- KIL 283
 181 IETGEERRLTFCHQGLSNVLDPKSAGVATFVLOEEFDRISGVWCPKAEITTSOG- KIL 240
 284 RILYEENDESEVEIIVHTSPMLSTRADSPFRYKGTGANPKVTFKKSEIMDAEGRIDV 343
 241 RILYEENDESEVEIIVHSPALERKTDSTRYRTSKNPKIALKAEFTDSOGKIVST 300
 344 IDKELIOPPEILFEGVEYIARAGWTPEGKYAMSILLDRSOTRLQIYLISELFIPEDDV 403
 301 QEKELVOPESSELPKVEYIARAGWTGDKYAMAMFLDRPOQIOLVLLPALIPSTENE 360
 404 MERQRLIESVDSVPTLLIYEETDIIMINIHDIHFVPOSH-EEIEFIFASCKGFRH 482
 361 EQLARARAVPRVOPVYIEEVTWMINHDIFFRPOSEGDELCFLANCKGFCF 420
 463 LKXITLSLESKYKRRSGGLPAPSDKCPKEIEIATTSGEVEVILGRHNSIQIDEVRLV 522
 421 LKXITVAVLSOGYDWESEPSGDEFCPIKEIEIATTSGEVEVILGRHNSIQIDEVRLV 480
 523 YFEGTDSPLEHLLHYVSVNPEGVTRLDRCYSHSCCISQHCDFIISKNSQKNPCVS 582
 481 YFEGTDRDPLEHLLHYVSVNPEGVTRLDRCYSHSCCISQHCDFIISKNSQKNPCVS 540
 583 LKXITSPEDPTCKTEFNATILDSAGLPDYPPPEIFSESTGTGLYMLTKKPHDLP 642
 541 VYKLSPPDDPLKOPRFVMSMMAASCPDYVPELIFHHTKSDVRLYGMITKPHALOP 600
 643 GKXYPVLEIYGGPOVOLVNNRKGKVFRLNTLASIGYVVVVINDRSGCHRLKEGAF 702
 601 GKXHPVLEIYGGPOVOLVNNRKGKVFRLNTLASIGYVVVVINDRSGCHRLKEGAF 660
 703 KYMGQIEIDDOVGLQIYASRYDFIDLRVGIHGSYGYLSLMAIMORSDFIRVAIAG 762
 661 KMGQIEIDDOVGLQIYASRYDFIDLRVGIHGSYGYLSLMAIMORSDFIRVAIAG 720
 763 APYTLFIPTDYGTERTYMGHPDQNEGGYVGSYVAMQAEKPEPSPNRLILHGLDENVHF 822
 721 APYTLFIPTDYGTERTYMGHPDQNEGGYVGSYVAMQAEKPEPSPNRLILHGLDENVHF 780
 823 AHTSILSFLVRAGKPDYDQIYPOERHSIRVPSEGEHYELHLLHYLOENL 872
 781 FHTNFIYSQILRAGKPDYDQIYPOERHSIRVPSEGEHYELHLLHYLOENL 830

RESULT 18

ID AAE24169 standard; Protein: 869 AA.

XX AAE24169;

DT 23-SEP-2002 (first entry)

Alternative version of murine dipeptidyl peptidase 9 (DPP9) protein.

Murine; dipeptidyl peptidase; DPP; neoplasia; cirrhosis; HIV infection; human immuno deficiency virus; graft rejection; cytostatic; autoimmunity; type II diabetes; antidiabetic; antiinflammatory; immunosuppressive; antiviral; enzyme.

Mus sp.

WO200234900-A1.

02-MAY-2002.

29-OCT-2001: 2001WO-AU01388.

27-OCT-2000: 2000AU-0001078.

(UNSY) UNIV SYDNEY.

Abbot CA, Correll MD;

WPI: 2002-45464/48.

N-PSDB: AAD38955.

New dipeptidyl peptidase (DPP) peptidase, useful for screening inhibitors of DPP catalytic activity, which may be employed to treat e.g. neoplasia, type II diabetes, cirrhosis, autoimmunity, graft rejection and HIV infection.

Claim 1: Page 70-74; 91pp: English.

The present invention relates to dipeptidyl peptidase (DPP) proteins and polynucleotides encoding such proteins. The DPP peptidase are useful for screening inhibitors of DPP catalytic activity. The inhibitors are useful for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft rejection and HIV (human immuno deficiency virus) infection. The present sequence is an alternative version of murine DPP9 protein.

Note: This sequence is stated to be the same as that shown as SEQ ID NO: 4 in the sequence listing of the specification. However these sequences differ.

Sequence 869 AA:

Query Match 60.3%; Score 2833; DB 23; Length 869;

Best Local Similarity 60.8%; Pred. No. 8.7e-264; Matches 511; Conservative 134; Mismatches 193; Indels 2; Gaps 2;

35 FVYERYSMSQLKRLADTRKHYGMMAKAPHDPEFKRNDPDRPHSDRIYLLAMSGENR 94
 30 FCYQKMSWDLRSITINGSRKSSGLIYVKAHPDFOVKOTDESGHSHRLYLCPGSRNS 89
 95 NTFYSEIPKTIIRAAVLMISMKPLDLFOATLDYGMYSREELLREKRIGTGVGASDY 154
 90 NSLTYSEIPKTIIRAAVLMISMKPLDLFOATLDYGMYSREELLREKRIGTGVGASDY 149
 155 YHOGSGTFLFQAGSGIYHVKDGGPGFTOOLPRNLVETSCPNIRMDPKLCPADPMIAE 214
 150 FHSSEGLFLFQASNSLFGHCRDGGKNGFVSPMKPLEIKTCQSGPRMDPKICPADPAFFSF 209
 215 IHSNDIWSNIVTRERRLTYVHNELANMEDARSAGVATFVLOEEFDRISGVWCPKAE 274
 210 INNSDLVANIETGEERRLTFCHQGSAGVADNPKSAGVATFVLOEEFDRISGVWCPKAE 269
 275 TTPSGG- KILRILYEENDESEVEIIVHTSPMLSTRADSPFRYKGTGANPKVTFKKSEIM 333
 270 WESSEGLTLRLIYEENDESEVEIIVHSPALERKTDSTRYRTSKNPKIALKAEFTDSOG 329
 334 IDAEGRIDVIDKELIOPPEILFEGVEYIARAGWTPEGKYAMSILLDRSOTRLQIYLISP 393
 330 TDHOGKIVSSCEKELVOPESSELPKVEYIARAGWTGDKYAMAMFLDRPOQIOLVLLPP 389
 394 ELFIPEDDVMERQRLIESVDSVPTLLIYEETDIIMINIHDIHFVPOSH-EEIEFIF 452

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DB 390 ALFPAVESEAAQAAARAVKNOPEVIEEVNWMVNHADIFHPQAOAGOODFCFLR 449
453 ASECCTGFRHLKYKTTSLIKESKYRRSSGGLPAPSDFCPIKEETALTSGEVIEVGRHNSN 512
450 ANECKTGCHLYKVTAVELKTKDYMTPELSTEEGFCPIKEEVALTSGEVIEVLSRHGSK 509
513 IOVEVRLVYFEGCTKDSPLEHLLVYVSYVNPGEVTRTLDRGYSHSCCISOCHDFISKY 572
510 IAWNQKRLVYFQGTGKDTPLHLLVYVSYESAGEIVRLTTGFSHSCMSQSFMEVSHY 569
573 SNOKNPHCVSLYKLSPEDDPTCKTEFWATILDSAGPLDPYTPPELTFSESTGFTLYG 632
570 SSVSTPPCVVHYKLSGDDPLHLLKQPRFMASSMAEAMPDYPVPELTFHFTRADVLYG 629
633 MLYRPHDLQPGKKPYTLFTFYIGSPVOVLVNNRFGVKYFRNLNTLASIGYVVVINDRSC 692
630 MLYRPHDLQPGKKPYTLFTFYIGSPVOVLVNNRFGVKYFRNLNTLASIGYVVVINDRSC 689
693 HRLGKEGAEFYKMGQIEIDDOVEGLOYLASRYDFIDLDRVGIHGSYGYLSMALMQR 752
690 QRGHFEKALKNQMGQYIEIDQVEGLQYVAEKYFIDLSRAVHIGWSYGFSLMGLIHK 749
753 SDIRVALIAGAPVTLMTFYDTGTERYMGHPDQDQGYLGSVAMQAEKFPSEPNRLLL 812
750 PÖVEKVALIAGAPVTVMAYDGYTERYMDVPENNQGYEAGSVALHVEKLPNEPNRLLL 809
813 HGFIDENVHFAHTSILSLFVLRACKPYDLOITYPOERHSIRPESGEHELHLYLOENL 872
810 HGFIDENVHFAHTSILSLFVLRACKPYDLOITYPOERHSIRPESGEHELHLYLOENL 869

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RESULT 19

ABG61607 standard; Protein; 879 AA.

AC ABG61607;

DT 12-AUG-2002 (first entry)

DE Human DPRP-2 splice variant #6.

Human: serine protease; dipeptidyl peptidase IV-related protein; DPRP; DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain; diabetes; infertility; obesity; anorexia; Parkinson's disease; stroke; heart failure; hypertension; urinary retention; osteoporosis; cancer; ulcer; allergy; cancer; psychotic disorder; neurological disorder; dyskinnesia; reproductive disorder; inflammatory disorder; metabolic disorder.

OS Homo sapiens.

PN MO200231134-A2.

PD 18-APR-2002

PF 12-OCT-2001; 2001MO-US31874.

PR 12-OCT-2000; 2000US-240117P.

PA (FERR) FERRING BV.

PI Q1 S, Akinsanya KO, Riviere PJ, Junien J;

DR WPI: 2002-444178/47.

DR N-PSDB; ABR83338.

New dipeptidyl peptidase IV-related proteins and nucleic acids encoding the proteins, useful for treating e.g. fungal, bacterial, protozoan and viral infections, cancers, allergies, neurological disorders, or pain

PS Disclosure; Page 91-93; 113pp; English.

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XX The present invention relates to the isolation of novel human serine
CC proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC and nucleic acids encoding them are useful for treating infections
CC such as fungal, bacterial, protozoan and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC stroke, ulcers, asthma, allergies, cancers, migraine, vomiting,
CC psychotic and neurological disorders (e.g. anxiety, dementia, or
CC schizophrenia), and dyskinnesia. These may also be used in discovering
CC therapeutic agents for the treatment of reproductive, inflammatory and
CC metabolic disorders. ABG61591-ABG61612 represent human DPRP proteins.
XX
SQ Sequence 879 AA;
Query Match 60.0%; Score 2820.5; DB 23; Length 879;
Best Local Similarity 60.7%; Pred. No. 1,4e-262;
Matches 510; Conservative 132; Mismatches 183; Indels 15; Gaps 3;
35 FVERYSWSOLKLLADTRKHGMAMKAPDPEVKNRNDPDGSHSDRIYLANSGEURE 94
53 FÖVQKHSWDGSLRSIHSRKYSGLIVNKAPDFOVOKTDESGHSHRLYGLMPYGSRE 112
95 NTLFYSEIPTINRAAVYLMISMKPLDLFOATLDYGMYSREELLRRKRIGTVIASYD 154
113 NSLYSELPKVKREKALLLSMKOMLDFQATPHHGYASREELLRRKRIGTVIASYD 172
155 YHOGSGTFLEFGAGSGLYHVKGDPQGFQOPLRPNLVETSCPNIRMDPKLCPADPMIAF 214
173 FHSSEGLFLEFQASNSLFRCDGKNGFVSPMKPLEIKTQCSGRMPDKICPADPAEFSE 232
215 IHSNDIMSNVTREERLTYVHNELANMEDASAGVATVLOEEDRYSGYWMCRAE 274
233 INNSDLWANLETEBERLTFCHOGLSNVLDPPKSAGVATVLOEEDRYSGYWMCRAE 292
275 TTPSGG-KILRLYEENDESEVEIIVHTSPMLERRADSFYPTGTANPKVTFKMEIM 333
293 WEGSEGLKTLRLILEYDEVEVEIIVHSPALBERKDSYVPTGTANPKVTFKMEIM 352
334 IDAEGRIIDVIDKELIOPFETLFEVGEVYIARAGWTPBEKAWMSILLDRSOTRIQVILSP 393
353 TDSOGKIVSTDEKELVOPFSSLPFKVEYIARAGWTPBEKAWMSILLDRSOTRIQVILSP 412
394 ELTFPVEDDWMERRLIESVDSVTPLIYEETDIMINIHIDIPHVPOSH-BEEIEEIF 452
413 ALFIPSTENEBÖRLASARAVERNÖPYVVEEVNWMVNHADIFPPÖSGEDELCPFLR 472
453 ASECCTGFRHLKYKTTSLIKESKYRRSSGGLPAPSDFCPIKEETALTSGEVIEVGRHNSN 512
473 ANECKTGCHLYKVTAVELKTKDYMTPELSTEEGFCPIKEEVALTSGEVIEVLSRHGSK 531
513 IOVEVRLVYFEGCTKDSPLEHLLVYVSYVNPGEVTRTLDRGYSHSCCISOCHDFISKY 572
532 -----KGTGDTPLHLLVYVSYEAGAEIVRLTTPGFSHSCMSQSFMEVSHY 579
573 SNOKNPHCVSLYKLSPEDDPTCKTEFWATILDSAGPLDPYTPPELTFSESTGFTLYG 632
580 SSVSTPPCVVHYKLSGDDPLHLLKQPRFMASSMAEAMPDYPVPELTFHFTRADVLYG 639
633 MLYRPHDLQPGKKPYTLFTFYIGSPVOVLVNNRFGVKYFRNLNTLASIGYVVVINDRSC 692
640 MLYRPHDLQPGKKPYTLFTFYIGSPVOVLVNNRFGVKYFRNLNTLASIGYVVVINDRSC 699
693 HRLGKEGAEFYKMGQIEIDDOVEGLOYLASRYDFIDLDRVGIHGSYGYLSMALMQR 752
700 QRGHFEKALKNQMGQYIEIDQVEGLQYVAEKYFIDLSRAVHIGWSYGFSLMGLIHK 759
753 SDIRVALIAGAPVTLMTFYDTGTERYMGHPDQDQGYLGSVAMQAEKFPSEPNRLLL 812
760 PÖVEKVALIAGAPVTVMAYDGYTERYMDVPENNQGYEAGSVALHVEKLPNEPNRLLL 819

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